Page 1

10/623567

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OM protein - protein search, using sw model

August 3, 2005, 21:41:13; Search time 165 Seconds (without alignments) 731.329 Million cell updates/sec Run on:

US-10-623-567A-1 1573 1 MANNDAVIKRLEQKGAEADQ......FEVKGKGVCRAQTMSNSGIK 312 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

2105692 segs, 386760381 residues .

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
4: geneseqp2001s:*
5: geneseqp201s:*
6: geneseqp2003as:*
7: geneseqp2003as:*
8: geneseqp2003bs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Abb07442 Human p43			Adp85653 Human end	Aab63244 Human bre							-	_	_		_		Novel		-	Human	Human			Adq65849 Novel hum
	αī	ABB07442	AA029575	ADH74487	ADP85653	AAB63244	AAR72577	ABU10452	ADS80906	AAW14561	ABU10250	ADS80904	ABB59210	ABM74361	ABM73655	ABU10451	ADS80905	AAE19811	ADN99968	ADN73157	AAB47611	AAE13487	ABU72380	ADF76697	ADN05830	ADQ65849
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* Query	Match	100.0	100.0	100.0	100.0	100.0	85.4	52.8	52.8	52.3	45.1	45.1	42.7	33.2	33.2	32.8	32.8	32.5	32.2	31.7	28.7	28.7	28.7	28.6	28.6	28.6
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	178	4	AAB47613	Aab47613	Human Tyr
	178	ហ	AAE13489	Aae13489	Human Tyr
	178	9	ABU72382	Abu72382	Human Tyr
	168	~	AAW06596	Aaw06596	Human end
	168	ო	AAY69674	Aay69674	Human end
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	389	m	AAG31612	Aag31612	
	440	e	AAG31611	Aag31611	Arabidops
	525	4	ABB60745	Abb60745	Drosophil
	265	7	ABM74280	Abm74280	DNA clone
	273	m	AAG08528	Aag08528	Arabidops
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	28	9	ABU72393	Abu72393	Human pro
	720	9	ADA33478	Ada33478	Acinetoba
225 14.3	069	ø	ABU16644	Abu16644	Protein e

ALIGNMENTS

Kim

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The present invention relates to novel differentially regulated genes and polypeptides encoded by them. Sequences of the invention are useful in diagnosing, staging, monitoring, prognosticating, preventing, treating or determining the predisposition to diseases or conditions such as prostate cancer. They may be used as molecular markers, drug targets, vaccines, in gene therapy, research, clinical medicine or forensic science. The present sequence is a differentially regulated prostate protein (endothelial monocyte activating polypeptide II), Pc240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide for diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining the predisposition to, diseases or conditions such as prostate cancer, and for research or forensic science.
                                      Human; differentially regulated protein; prevention; therapy; vaccine; prostate cancer; endothelial monocyte activating polypeptide II; gene therapy; Pc240.
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Best Local Similarity 100.0%; Pred. No. 1.6e-135;
Matches 312; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Fan W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 183-184; 100pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                          Kovacs KF,
                                                                                                                                                                                                                                                                                                                                                                                                 (ORIG-) ORIGENE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                          07-NOV-2001; 2001US-0331041P.
07-NOV-2001; 2001US-0331042P.
18-DEC-2001; 2001US-034025-P.
07-JAN-2002; 2002US-0344791P.
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N-PSDB; AAL60070.
Human Pc240 protein.
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                                                                                                                                                                 WO2003040331-A2
                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides an anti-tumour and anti-angiogenic agent of p43 consisting of two domains, the N-terminal domain (146 amino acids) and cterminal domain (166 amino acids) containing 11 beta-strands forming a structural core and 3 flanking alpha-belices. p43 is useful as an anti-tumour and anti-angiogenic agent. p43 and its C-terminal cytokine domain (EMAP II) induce regression of fibrosarcoma in immunocompromised mouse while its N-terminal domain does not. p43 is a potent cytokine as determined by the induction of tumour necrosis factor-alpha (TMP-alpha), interleukin-6 (IL-6), IL-8 and matrix metalloprotease-9 or by its activity of chemotaxis. The present sequence represents the human p43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                     Novel anti-tumor and anti-angiogenic agent of p43 comprises N-terminal domain and C-terminal domain containing eleven beta-strands forming a structural core and three flanking alpha-helices.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
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100.0%; Pred. No. 1.6e-135;
iive 0; Mismatches 0;
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                           WPI; 2002-098017/13.
                                                                                                                                                                                                                                                                                              N-PSDB; ABA94640.
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                                                                                                                                                                                                                                  Κο Υ,
                       WO200195927-A1
                                                                20-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide
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Length 312; Indels 120

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RESULT

(first entry)

27-AUG-2003

AA029575;

AAO29575 ID AAO2 XX AC AAO2 XX DT 27-P

RESULT

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181 VGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA 240
                                                             241 PPNGSVPGDRITFDAPPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New oligonucleotide compound that inhibits expression of EMAP-II, useful for preparing a composition for treating hyperproliferative disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMAP-II; endothelial monocyte-activating polypeptide-II; EMAP-2; SCYEI; small inducible cytokine subfamily E member 1; hyperproliferative disorder; cancer; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                     Human endothelial monocyte-activating polypeptide-II (EMAP-II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 22-23; 35pp; English.
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                                                                                                                                                                                                                                                                           ADP85653 standard; protein; 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-DEC-2002; 2002US-00316232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRAQTMSNSGIK 312
                                                                                                                                                                      301 CRAOTMSNSGIK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bennett CF, Dean NM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-440333/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADP85584.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2004110144-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                26-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g. cancer
                                                                                                                                                                                                                                                                                                                      ADP85653;
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                                             241
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                                                                                                                                                                                                                                                              ADP85653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the use of one or more polypeptides (I) chosen from a polypeptide having a fully defined p43 sequence of 312 amino acids a given in the specification and a polypeptide having 70% to more capture homology with (S1), for the manufacture of the pharmaceutical composition (II) which is intended to stimulate wound healing in a subject. The pharmaceutical composition (II) which is intended to stimulate wound healing in a subject. The wound is chosen from burn, ulcer, trauma, post-surgical, post-child birth, chronic wound and dermatitis. The burn is chosen from sun burn, chemical burn, radiation burn, and thermal burn. The ulcer is chosen from pressure ulcer, plaster ulcer and decubitus ulcer. The chronic wound is chosen from bedsores, pressure sores, clicknessetes-related and poor circulation-related. The dermatitis is chosen from impetigo, intertrigo, follicultiis and ecasema. The current sequence represents the wound healing stimulating polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p43 polypeptide, for the manufacture of pharmaceutical composition of to stimulate wound healing in a subject.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 KKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MANNDAVLKRLEGKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE 60
                                                                                                                                                                                          Vulnerary; antiulcer; dermatological; antiallergic; antiinflammatory; wound healing; burn; ulcer; trauma; post-surgical; post-child birth; chronic wound; dermatitis; sunburn; chemical burn; radiation burn; thermal burn; pressure ulcer; plaster ulcer; decubitus ulcer; bedsores; pressure sore; diabetes; poor circulation; impetigo; intertrigo; folliculitis; eczema; p43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
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                                                                                                                                                    Human wound healing stimulating polypeptide p43, SEQ ID 1.
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100.0%; Pred. No. 1.6e-135;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1; 20pp; English.
                            ADH74487 standard; protein; 312 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYSE-) UNIV SEOUL NAT IND FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUL-2003; 2003EP-00016724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUL-2002; 2002KR-00042858.
                                                                                                             (first entry)
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Matches 312; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-145613/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 312 AA;
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                      EP1384486-A1
                                                                                                             15-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JAN-2004
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120
The present invention relates to a compounds, compositions and methods for modulating the expression of endothelial monocyte-activating polypeptide-II (BMAP-II). EMAP-II is also known as EMAP-2, small inducible cyckine subfamily E, member 1 (SCYEI). The compound comprises antisense oligonucleotides targetted to EMAP-II. The invention is useful for preparing a composition for treating hyperproliferative disorder e.g. cancer. It is also useful in gene therapy. The present sequence is human endothelial monocyte-activating polypeptide-II (EMAP-II). This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 KKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELKOELIQAEIQNGVKOIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE
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A mouse methA sarcoma cDNA library was screened with a probe based on the N-terminal sequence of mouse EMAPII. Overlapping clones were combined to obtain a contiguous full-length sequence (given in AAQ86718) encoding a 33 kDa protein (AAR72577). Recombinant EMAPII was expressed in E. coli. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New endothelial monocyte activating polypeptide II - induces chemotaxis, inflammation and tissue factor, useful for treating tumours, also related antibodies, DNA and active fragments.
                                ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE
                 ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE
                                                                                            KKAKEKI EKKGEKKEKKOOSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVD
                                                                                                                                                     1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
                                                                            KKAKEKI EKKGEKKEKKQQSI AGSADSKPI DVSRLDLRI GCI I TARKHPDADSLYVEEVD
                                                                                                                                    VGEIAPRIVVSGLVNHVPLEOMONRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA
                                                                                                                                                                                                 PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV
                                                                                                                                                                                                              PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMAPII; endothelial monocyte activating polypeptide II; chemotaxis; inflammation; tissue factor; tumor; cancer; therapy; methA; sarcoma.
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llarity 85.9%; Pred. No. 2e-114;
Conservative 13; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kayton M, Libutti SK;
                                                                                                                                                                                                                                                                                                                                                                  AAR72577 standard; protein; 310 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 4; 180pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                              CRAQTMSNSGIK 328
                                                                                                                                                                                                                                                           CRAQTMSNSGIK 312
                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1995-147389/19.
N-PSDB; AAQ86718.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse EMAPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9509180-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-SEP-1994;
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Best Local Simi:
Matches 269; (
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29-SEP-1995
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                                                                                                                                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleic acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein,
VGEIAPRIVVSGLVMHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA 240
                                                                                                          PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV 300
                                                                                                                         241 PPNGSVPGDRITFDAPPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV 300
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                                                            Human breast cancer associated antigen protein sequence SEQ ID NO:606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding breast, gastric and prostate cancer associated antigen precursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63360
                                                                                                                                                                                                                                                                                                                                                                                              Human; breast cancer; gastric cancer; prostate cancer; diagnosis;
cancer associated antigen; cytostatic; cancer vaccine.
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100.0%; Pred. No. 1.7e-135;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 478; 799pp; English.
                                                                                                                                                                                                                                                                           AAB63244 standard; protein; 328 AA.
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99US-0153454P.
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                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                   CRAQTMSNSGIK 312
                                                                                                                                                                                                 CRACTMSNSGIK 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200073801-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                    26-MAR-2001
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Matches 312;
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                                                                                                                                                                                                                                                                                                     AAB63244;
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The present invention relates to a method of enhancing an immune response. The method involves administering an immunological enchancement agent having the N-terminal domain of p43 protein to a cell or tissue. The invention is useful for enhancing an immune response with an immunological enhancement agent in apoptotic disorders such as cancer. The present sequence is the mammalian p43(91-256) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MYSENVIQSTAVTTVSSGTKEQIKGGTGDEKKAKEKIEKKGEKKEKKQQSIAGSADSKPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enhancing an immune response using an immunological enhancement agent having the N-terminal domain of the p43 protein, useful in apoptotic
                                                                                                                                                                                                                                                                                                                                                                             Immune response; p43; apoptotic disorder; cancer; cytostatic; immunostimulant; cytokine-agonist.
                                                                                                                      211 CNLKPAKMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAF 256
                                                                                                                                           CNLKPAKMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CNLKPAKMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.8%; Score 831; DB 8; I
100.0%; Pred. No. 7.8e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 7.8
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 3; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.00
100.08; Fig.
                                                                                                                                                                                                                                               ADS80906 standard; protein; 166
                                                                                                                                                                                                                                                                                                                                               Mammalian p43(91-256) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-APR-2004; 2004US-00823730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-2001; 2001KR-00031310.
16-AUG-2001; 2001US-00930169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMAG-) IMAGENE CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-689153/67.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2004185060-A1
                                                                                                                                                                                                                                                                                                               16-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-SEP-2004
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                                                                                                                                                                                                                                                                             ADS80906;
                                                          151
                                                                                         61
                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia
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                                                             239
                                                                                                                                                                                                APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKG 299
                                                                                                                                                                                                                                                                 EKKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEV 179
          MATNDAVLKRLEQKGAEADQIIEYLKQQVALLKEKAILQATMREEKKLRVENAKLKKEIE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New immunological enhancement agent comprising an N-terminal peptide of p43, useful for increasing the amount of tumor necrosis factor and interleukin-8 to improve the immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents an immunological enhancement agent comprising an N-terminal peptide of p43. The peptide can act as a cytokine to increase the amount of tumour necrosis factor (TNP) and interleukin-8 useful for improving an immune response and used as an immunological enhancement agent. The present sequence represents the amino acid sequence of the immunological enhancement 3901. The present sequence represents the
                                          ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAV-TTVSSGTKGQIKGGTGD
                                                                                                                                                                              DVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agonist; p43; cytokine; interleukin-8; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.8%; Score 831; DB 6; Length 166; 100.0%; Pred. No. 7.8e-68; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunological enhancement agent p43 (91-256)
                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU10452 standard; protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3, Page 5, 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-AUG-2001; 2001US-00930169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-2001; 2001KR-00031310
                                                                                                                                                                                                                                                                                                                                      VCRAQTMANSGIK 310
                                                                                                                                                                                                                                                                                                                    VCRAQTMSNSGIK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour necrosis factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-447359/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US2003004309-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ko Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-2003
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Length 166; Indels 150

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256 166

91 MVSENVIQSTAVTTVSSGTKEQIKGGTGDEKKAKEKIEKKGEKKEKKQQSIAGSADSKPI 150

Query Match Best Local S

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim S,
                                                                                                                          RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A method has been developed for the treatment of tumours. The method involves subcutaneous, intravenous, intravenous administration of an endothelial monocyte activating sequence represents murine EMAP-II which can be used to produce the EMAP-II derived polypeptide as long as it contains at least ninety percent homology to the present sequence. The method is especially used to treat carcinoma (administered intraperitoneally) or glioblastoma (administered intravenourally by positive pressure microinfusion). Inhibition of endothelial cell growth is particularly applied to acritic cells and inhibition of angiogenesis to treatment of eye diseases associated with excessive blood vessel formation, especially retinopathy (diabetic, related to sickle cell anaemia, retinopathy of prematurity or age-related macular degeneration). Intraperitoneal administration allows tumours too
                                                                                                                                             EMAP-II; inhibitor; endothelial cell formation; blood vessel; retinopathy; tumour; subcutaneous; intraperitoneal; intravenous; intracranial; intratumoural; carcinoma; glioblastoma; positive pressure microinfusion; aortic cell; angiogenesis; eye disease; diabetes; sickle cell anaemia; prematurity; age-related macular degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treatment of tumours with endothelial monocyte activating peptide II - also used to inhibit growth of endothelial cells and formation of blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                over 2 mm in diameter) for intratumoural injection to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.3%; Score 823; DB 2; Length 166; Best Local Similarity 93.9%; Pred. No. 4.2e-67; Matches 155; Conservative 5; Mismatches 5; Indels
                                                                                                                          Endothelial monocyte activating polypeptide II.
                                                                                                                                                                                                                                                                                                           label= Ser, Met, Gly
                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                        AAW14561 standard; protein; 166 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 13; Page 73; 104pp; English
                                                                                                                                                                                                                                                                                                                                     /label= Cys, Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               treated before they grow larger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vessels, e.g. in retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0003898P.
                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-US015007
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schwarz M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-202617/18.
                                                                                                                                                                                                                                                                                                                         Misc-difference 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 166 AA;
                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                         18-SEP-1996;
                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-SEP-1995;
                                                                                                01-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                               27-MAR-1997
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                                                                   AAW14561;
             RESULT 9
                             AAW14561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New immunological enhancement agent comprising an N-terminal peptide of p43, useful for increasing the amount of tumor necrosis factor and interleukin-8 to improve the immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents an immunological enhancement agent comprising an N-terminal peptide of p43. The peptide can act as a cytokine to increase the amount of tumour necrosis factor (TNF) and interleukin-8 useful for improving an immune response and used as an immunological enhancement agent. The present sequence represents the amino acid sequence of the immunological enhancement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
                                                                                                                                                                                                                                                                                                                                                                                                                             Immunostimulant; cytokine agonist; p43; cytokine; interleukin-8; TNF;
tumour necrosis factor.
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                                                                        KKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQTMSNSGIK 312
                                                                                              KKIWEQIQPDLHTNAECVATYKGAPFEVKGKGVCRAQTWANSGIK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.1%; Score 709; DB 6; Lv
100.0%; Pred. No. 1e-56;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                     Immunological enhancement agent p43 (1-147)
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                                                                                                                                                                                                                                            ABU10250 standard; protein; 147
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Matches 147; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US2003004309-A1.
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                                                                        268
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RESULT 11

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148 KPIDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRMV 207

KPIDASRLDLRIGXIVTAKKHPDADSLYVEEVDVGEAAPRTYVSGLVNHVPLEQMQNRWV

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ADS80904

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL4016176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIQAEIQNGVKQIAFP-----SGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEKKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 VDVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ADLQQIASNNERAEALINSIEAEISGIQQ----QLVERQKQELIKENAALAKEVEAALAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAPPNGSVPGDRITFDAFPGBPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFBVKGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 AVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIEELKQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 4422; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.7%; Score 671; DB 4;
44.9%; Pred. No. 8.6e-53;
ative 57; Mismatches 88.
                                                                                                                                                                                                                                         Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABM74361 standard; protein; 280 AA
                                                                                                                                                                                                                                           PWD,
                                                                                                                                                23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150
                                                                                                           23-MAR-2001; 2001WO-US009231
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Drosophila melanogaster.
                                                                                                                                                                                                                                           Adams M,
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                                   WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                              interactions
                                                                                                                                                                                                                                         Venter JC,
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method of enhancing an immune response. The method involves administering an immunological enchancement agent having the N-terminal domain of p43 protein to a cell or tissue. The invention is useful for enhancing an immune response with an immunological enhancement agent in apoptotic disorders such as cancer. The present sequence is the mammalian p43(1-147) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enhancing an immune response using an immunological enhancement agent having the N-terminal domain of the p43 protein, useful in apoptotic disorders such as cancer.
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                                                                                                                                                Immune response; p43; apoptotic disorder; cancer; cytostatic;
immunostimulant; cytokine-agonist.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.1%; Score 709; DB 8; Length 14
100.0%; Pred. No. 1e-56;
ive 0; Mismatches 0; Indels
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   ADS80904 standard; protein; 147
                                                                                                                                                                                                                                                                                                                                                          05-JUN-2001; 2001KR-00031310.
16-AUG-2001; 2001US-00930169.
                                                                                                              Mammalian p43(1-147) protein.
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Best Local Similarity 100.
Matches 147; Conservative
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                                        ADS80904;
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Length 294;

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17-OCT-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to oligonucleotide clones originating in barley (Hordeum vulgare) which contain single nucleotide polymorphisms (SNP). The oligonucleotides may be used for analysis of SNPs among barley varieties, identification of particular varieties and genotype-phenotype analysis, isolation of specific genes and creation of new varieties by transformation of barley varieties with them and production of new barley varieties with desired properties. The present sequence represents an oligonucleotide clone sequence featured in the specification. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTPLHANSMVSENVIQSTAVTTVSSGTKEQIKG-GTGDEKKAKEKIEKKGEK----KEK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 GKPVPLFKELKDQEVBAFRIKFAGSQAERILKGQADAEAKKVAEKL--KGTKLSEGSSKK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNH 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 VPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPE--KIEILAPPNGSVPGDRITFD 254
                                   Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 AFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQTMSNSGIK 312
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barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77; Indels 11;
                                                                                                                                                                                                                                                                                                          Single nucleotide polymorphism sites in barley varieties and I sequences containing them for analysis and identification of karieties and production of barley transformants with desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.2%; Score 522.5; DB 7; Length 280; 45.4%; Pred. No. 3.4e-39; tive 42; Mismatches 77; Indels 11
            ONA clone originating in barley containing SNP sequence #771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published-pct-sequences
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID XX; 284pp; Japanese.
                                                                                                                                                          20-DEC-2001; 2001JP-00387059.
20-DEC-2001; 2001JP-00387131.
20-DEC-2001; 2001JP-00403299.
20-DEC-2001; 2001JP-00403309.
27-SEP-2002; 2002JP-00327515.
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                                                                                                                                    2002WO-IB005403
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108; Conserva
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                                                                                    WO2003057877-A1:
                                                           Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                               characteristics
                                                                                                                                    16-DEC-2002;
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Best Local Si
Matches 108
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ABM73655 standard; protein; 289

ABM73655

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                                                     Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
barley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Single nucleotide polymorphism sites in barley varieties and I sequences containing them for analysis and identification of k varieties and production of barley transformants with desired characteristics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 289;
DNA clone originating in barley containing SNP sequence #65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.2%; Score 522.5; DB 7;
45.4%; Pred. No. 3.5e-39;
iive 42; Mismatches 77;
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                                                                                                                                                                                                                                                                                                                                    2001JP-00387059.
2001JP-00387131.
2001JP-00403299.
2001JP-00403300.
2002JP-00327515.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYNI-) UNIV JAPAN OKAYAMA
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Matches 108; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 289 AA;
                                                                                                             Hordeum vulgare
                                                                                                                                                                  WO2003057877-A1
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20-DEC-2001;
20-DEC-2001;
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New immunological enhancement agent comprising an N-terminal peptide of p43, useful for increasing the amount of tumor necrosis factor and interleukin-8 to improve the immune response.
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                                                                  Immunostimulant; cytokine agonist; p43; cytokine; interleukin-8; TNF; tumour necrosis factor.
                                          Immunological enhancement agent p43 (1-108).
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 5; 12pp; English
                                                                                                                                                                                                    16-AUG-2001; 2001US-00930169
                                                                                                                                                                                                                                 05-JUN-2001; 2001KR-00031310.
               (first entry)
                                                                                                                                                                                                                                                                                                                                    WPI; 2003-447359/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 108 AA;
                                                                                                                                             US2003004309-A1.
                                                                                                                                                                                                                                                            (KIMS/) KIM S. (KOYY/) KO Y.
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                                                                                                                                                                         02-JAN-2003.
               01-AUG-2003
                                                                                                                Mammalia.
                                                                                                                                                                                                                                                                                                       Kim S,
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1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE 60 Gaps ; 0 32.8%; Score 516; DB 6; Length 108; 100.0%; Pred. No. 3.4e-39; Live 0; Mismatches 0; Indels Query Match
Best Local Similarity 100.
Matches 108; Conservative ò

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Search completed: August 3, 2005, 21:54:21 Job time: 168 sec8

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Sequence 2, Appli Sequence 2751, Ap Sequence 21554, Ap Sequence 21654, Ap Sequence 17566, Ap Sequence 3507, Ap Sequence 4, Appli Sequence 7643, Ap Sequence 7643, Ap Sequence 19, Appli Sequence 11535, Ap Sequence 11535, Ap

BLOSUM62

Scoring table:

Perfect score:

6

Sequence:

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GENERAL INFORMATION:
Patent No. 6228837
GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Kao, Janet
APPLICANT: Kao, Janet
APPLICANT: Kao, Janet
APPLICANT: Steven K
TITLE OF INVENTION: Endothelial Monocyte Activating
TITLE OF INVENTION: Polypeptide II: A Mediator Which Activates Host Response
NUMBER OF SEQUENCES:
ADDRESSEE: Cooper & Dunham, LLP
COORESPONDENCE ADDRESS:
COOPER & Dunham, LLP
COOPER & Dunham, LLP
COOPER & Dunham, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-252-991A-21654
US-09-489-099A-8243
US-09-252-991A-17566
US-09-540-236-3507
US-08-844-059-4
US-09-431-202-4
US-09-543-681A-5403
US-09-543-681A-7643
US-09-134-078-19
                                                                                                                                                                                    PCT-US93-03077-3
US-09-949-016-11535
PCT-US93-03077-1
US-09-949-016-6596
US-09-949-016-10404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1185 Avenue of the Americas CITY: New York COUNTRY: USA ZIP: 1001
                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                      JS-08-360-821B-36
152.5
152.5
152.5
147
134.5
128
128
128
119.5
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116.5
116.5
116.5
116
 10, Appl
1, Appli
1, Appli
132, App
19812, A
                                                                                                                  (without alignments)
554.536 Million cell updates/sec
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                                                                                                                                                            US-10-623-567A-1 .
1573
1 MANNDAVLKRLEQKGAEADQ......FEVKGKGVCRAQTMSNSGIK 312
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Sequence 1
Sequence 1
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Sequence 1
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                                                                                                   August 3, 2005, 21:47:49 ; Search time 42 Seconds
                                                                                                                                                                                                                                                                                               513545
                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgm2_6/ptcdata/1/iaa/5A_COMB.pep:*
/cgm2_6/ptcdata/1/iaa/5B_COMB.pep:*
/cgm2_6/ptcdata/1/iaa/6A_COMB.pep:*
/cgm2_6/ptcdata/1/iaa/6B_COMB.pep:*
/cgm2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
/cgm2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-360-821B-36
US-09-851-026-36
US-09-9456A-37
US-08-129-456A-37
US-08-129-456A-37
US-09-129-456A-37
US-09-129-456A-37
US-09-129-456A-3
US-08-360-821B-35
US-08-360-821B-35
US-08-851-026-35
US-08-81-02-456A-11
US-08-919-039-132
US-09-919-039-132
US-09-919-039-132
US-09-123-615-1
US-09-123-615-1
US-09-123-615-1
US-09-123-615-1
US-09-123-615-1
US-09-123-615-1
US-09-123-615-1
US-09-123-615-1
US-09-123-615-1
                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                513545 segs, 74649064 residues
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                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                   Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                   Issued Patents AA:*
                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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Database

9 1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE Gaps .; 0 Query Match
99.7%; Score 1568; DB 3; Length 312;
Best Local Similarity 99.7%; Pred. No. 2.9e-136;
Matches 311; Conservative 0; Mismatches 1; Indels ò

MOLECULE TYPE: peptide

US-08-360-821B-36

4765, Ap 6201, Ap 4, Appli

Sequence

188.5 186.5 184 182.5 174.5

Sequence Sequence

2, Appli

Sequence

Sequence Sequence Sequence Sequence

US-09-248-796A-19813

1568 1568 1568 1510 1343 1343 1343

Result

Sequence

TOPOLOGY: linear

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Sequence 7144, Application US/09949016
; Sequence 7144, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TURENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR PLING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FeatSEQ for Windows Version 4.0
; SEQ ID NO 7144
LENGTH: 20
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                                                                                                    1 MANNDAVLKRLEGKGABADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
                                                                                                                                                                                                                                                                                                                VGEI APRIVVSGI VNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA
                                                                                                                                                                                                                                                                                                                                        9 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
                                                                               1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
                                                                                                                                                         ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE
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                                        Indels
Score 1568; DB 4;
Pred. No. 2.9e-136;
0; Mismatches 1;
Query Match
Best Local Similarity 99.7%;
Matches 311; Conservative
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Best Local Similarity 99.7
Matches 311; Conservative
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US-09-949-016-7144
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Kao, Janet
Kayton, Mark
Kayton, Mark
Libutti, Steven K
Libutti, Steven K
TITLE OF INVENTION: Endothelial Monocyte Activating
Polypeptide II: A Mediator Which Activates Host Response
                                                                                                                                                                                                                                          181 VGETAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA 240
                                                                                 ELKQELIQAEIQNGVKQIPPPSGTPLHANSNVSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
                                                                                                                                                             121 KKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVD 180
                                                                                                                                                                                                                      VGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIBILA 240
                                                                                                                                                                                                                                                                                                                    241 PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV 300
                                                                                                                                          KKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVD 180
                                                                                                                                                                                                                                                                                                  PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV 300
CUMPUTATIONS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PPC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.30, Version #1.30
CURRENT APPLICATION DATE: US/09/851,026
FILING DATE: 07-May-2001
CLASSIFICATION: «UMADOWN.»
PRIOR APPLICATION: «UMADOWN.»
PRIOR APPLICATION: UNMBER: US/08/360,821
FILING DATE: 08-OCT-96
ATPONEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION: UMMBER: 28,678
REGISTRATION: WIMPER: 28,678
REGISTRATION: WIMPER: 28,678
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ȚELECOMMUNICATION INFORMATION:

TELEPROME: 212-278-0400

TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, Lide
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-851-026-36
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SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 36, Application US/09851026; Patent No. 6734168; GENERAL INFORMATION: APPLICANT: Stern, David M. Clauss, Matthias
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US-09-851-026-36
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                                                                                          238 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKG 297
                                                             240 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKG 299
178 DVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEIL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MANNDAVLKRIEGKGAEADGIIEYLKOQVSLLKEKAILGATLREEKKLRVENAKLKKEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.4%; Score 1343; DB 1; Length 310; 85.9%; Pred. No. 1.5e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:

APPLICANT: Stern, David M.
APPLICANT: Clauss, Matthias
APPLICANT: Clause, Janet
APPLICANT: Kayton, Mark
TYPLICANT: Kayton, Mark
APPLICANT: Libutti, Steven K.
TITLE OF INVENTION: Endothelial-Monocyte Activating
TITLE OF INVENTION: Polypeptide II: A Mediator Which
TITLE OF INVENTION: Activates Host Response
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0 Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/129,456A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 36, Application US/08129456A; Patent No. 5641867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 29-SEP-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFRENCE/DOCKET NUMBER: 4173
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 278 0400
TELEPHAX: 212 391 0526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-SEP-1993
                                                                                                                                                                                                                               298 VCRAQTMSNSGIK 310
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Best Local Similarity 85.9
Matches 269; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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STATE: New York
COUNTRY: USA
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US-08-129-456A-36
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US-08-129-456A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 EKKAKEKIEKKGEKK-KKQQSIAGSADSKPIDASKLDLRIGCIITARKHPDADSLYVEEV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVGEIAPRTVVSGLVMHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEIL 239
                                          PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV 300
                                                                                249 PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MANNDAVLKRLEQKGAEADQIIBYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
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                                                                                                                                                                                                                           us-08-129-456A-37

Sequence 37, Application US/08129456A

Patent No. 5641867

GENERAL INFORMATION:

APPLICANT: Stern, David M.

APPLICANT: Clauss, Matthias

APPLICANT: Kao, Janet

APPLICANT: Libutti, Steven K.

TITLE OF INVENTION: Endothelial-Monocyte Activating

TITLE OF INVENTION: Polypeptide II: A Mediator Which

TITLE OF INVENTION: Activates Host Response

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: COODER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTAY: USDAY

ZUE: 10036

ZUE: 10036

COMBUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: PatentIn Release #1.0 Version #1.30

SOFTWARE: PatentIn Release #1.0 Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,456A
FILING DATE: 29-SEP-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
MAME: White, John P.
REGISTRATION NUMBER: 28,678
FREERENCE/DOCKET NUMBER: 41735
FELECOMMUNICATION INFORMATION:
TELEFAX: 212 391 0526
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acide

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TELENTH AND ACIDE TEMPLE TO ACIDE
TELEGH AND ACIDE
TELEGH AND ACIDE TEMPLE TO ACIDE TEMPLE
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Matches 306; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-129-456A-37
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61 ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAV-TTVSSGTKEQIKGGTGD 119
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                                                                                                180 DVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEIL 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MANNDAVLKRLEGKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE 60
                                                                              240 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFFVKGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Au-Young, Janice
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.9%; Score 1343; DB 3;
85.9%; Pred. No. 1.5e-115;
iive 13; Mismatches 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,615
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFILING DATA:

APPLICATION DATA:

APPLICATION NUMBER: 08/705,868

FTILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 35,749

REFERENCE/DOCKET NUMBER: PF-0117

TELECOMMUNICATION INFORMATION:

TELEPAK: 415-845-055

INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

LENGTH: 310 amino acids

TYPE: amino acids
                                                                                                                                                                                                                                                                                             ; Sequence 3, Application US/09123615; Patent No. 6090377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                        300 VCRAQTMSNSGIK 312
                                                                                                                                                                                              298 VCRAOTMANSGIK 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.94
Matches 269; Conservative
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ZIP: 94304
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61 ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAV-TTVSSGTKEQIKGGTGD 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Gaps
                                                                                                                                                                                                                                                             APPLICANT: Bandman, Olga
APPLICANT: Coleman, Roger
APPLICANT: Au-Young, Janice
APPLICANT: Murry, Lynn B.
TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
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85.9%; Pred. No. 1.5e-115;
iive 13; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,868
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0117 US
TELECHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
                                                                                                                                                                                                                                                 'US-08-705-868-3
; Sequence 3, Application US/08705868
; Patent No. S085798
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Coleman, Roger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                            298 VCRAQTMANSGIK 310
                                                                                                                                      VCRAQTMSNSGIK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 85.94
Matches 269, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
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Kao, Janet
Kayton, Mark
Kayton, Mark
Libutti, Steven K
TITLE OF INVENTION: Endothelial Monocyte Activating
Polypeptide II: A Mediator Which Activates Host Response
NUMBER OF SEQUENCES: 42
                                                                                                               240 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKG 299
                                                                                                                                                                                           DVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEIL 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 85.4%; Score 1343; DB 4; Length 310; Best Local Similarity 85.9%; Pred. No. 1.5e-115; Matches 269; Conservative 13; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: TADPO ALEA
COMPUTER: IN PUCCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30, Version #1.30
CURSUT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,026
FILING DATE: 07-May-2001
CLASSIPICATION: -UNKnown>
PRIOR APPLICATION: -UNKnown>
PRIOR APPLICATION: -UNKnown>
PRILING DATE: 08-OCT-96
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTERATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
TELECOMMINICATION INFORMATION:
TELEPRAX: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: peptide
, SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-851-026-35
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 35, Application US/09851026; Patent No. 6734168
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clauss, Matthias
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Stern, David M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                       300 VCRAQTMSNSGIK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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APPLICANT: Clauss, Matthias
APPLICANT: Clauss, Matthias
APPLICANT: Kao, Janet
APPLICANT: Kayton, Mark
APPLICANT: Libutti, Steven K
TITLE OF INVENTION: Endothelial Monocyte Activating
TITLE OF INVENTION: Polypeptide II: A Mediator Which Activates Host Response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAV-TTVSSGTKEQIKGGTGD 119
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                                                                                                  DVGEAAPRTVVSGLVNHVPLEOMONRMVVLLCNLKPAKMRGVLSQAMVMCASSPEKVEIL 237
                                                                                                                                                        240 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKG 299
                                                                                                                                                                                     238 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNAECVATYKGAPFEVKGKG 297
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EKKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEV 179
                    1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.30, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/360,821B FILING DATE: 08-OCT-96 CLASSIFICATION: 435 (TIONNES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.4%; Score 1343; DB 3;
85.9%; Pred. No. 1.5e-115;
tive 13; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Cooper & Dunham, LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 20
                                                                                                                                                                                                                                                                                                                                                                        Sequence 35, Application US/08360821B; Patent No. 6228837; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4173:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAK: 212-391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 310 aning acids
                                                                                                                                                                                                                                      300 VCRAQTMSNSGIK 312
                                                                                                                                                                                                                                                                             298 VCRAQTMANSGIK 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & STREET: 1185 Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-360-821B-35
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207 VILLCNLKPAKWRGVLSQAWVMCASSPEKIEILAPPNGSVPGDRITFDAFPGEPDKELNP 266
                                                                                                                                                                                            250 RITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQTMSNS 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SKPIDASRLDLRIGCIVTAKKHPDADSLYVEEVDVGEAAPRTVVSGLVNHVPLEQMQNRM 60
                                                              61 VSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVKSQAMVMCASSPEKIEILAPPNGSVPGD
                                 190 VSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILAPPNGSVPGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08129456A

Patent No. 5641867

GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Clauss, Matchias
APPLICANT: Kao, Janet
APPLICANT: Kao, Janet
APPLICANT: Libutti, Steven K.
TITLE OF INVENTION: Endothelial-Monocyte Activating
TITLE OF INVENTION: Polypeptide II: A Mediator Which
TITLE OF INVENTION: Activates Host Response
NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
ADDRESSEE: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIn PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0 Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/129,456A
FILING DATE: 29-SEP-1993
CLASSIFTCATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.1%; Score 835; DB 1; 94.0%; Pred. No. 3.9e-69; iive 6; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: White, John P. REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41735
TELECOMMUNICATION INPORMATION:
TELEPAX: 212,278 0400
TELEPAX: 213,391 0526
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 166 amino acids
amino acid
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Best Local Similarity 94.0
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New York
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: New York
                                                                                                                                                                                                                                                                                         310 GIK 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                        181
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                                                                                                                                                                                                                                                                                                                                                               DVGEAAPRIVVSGLVNHVPLEQMQNRMVVLLCNLKPAKMRGVLSQAMVMCASSPEKVEIL 237
                                                              61 ELKOELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAV-TTVSSGTKEQIKGGTGD 119
                                                                                                   120 EKKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEV 179
                                                                                                                                                                                                                              180 DVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEIL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MATNDAVLKRLEGKGAEADQIIEYLKQQVALLKEKAILQATMREEKKLRVENAKLKKEIE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 KGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08483534A

| Patent No. 6013483
| GENERAL INFORMATION:
| APPLICANT: Rosen, Craig
| TITLE OF INVENTION: Endochelial-Monocyte Activating
| TITLE OF INVENTION: Polypeptide III
| NUMBER OF SEQUENCES: 7
| CORRESPONDENCE ADDRESS: ADDRESSE: CARCILLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN
| STREET: 6 BECKER FARM ROAD | STREET: NOSELAND
| STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOSELAND | STREET: NOS
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MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: 18M PS/2
CURRENT APPLICATION DATA:
CLASSIFICATION NUMBER: 05/08/483,534A
FILLING DATE: 07/3UN 95
CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 33,073
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 201-994-1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||||||:|||||
VCRAQTMANSGIK 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300 VCRAQTMSNSGIK 312
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Matches 180, Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: PROTEIN
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Libutti, Steven K
TITLE OF INVENTION: Endothelial Monocyte Activating
Polypeptide II: A Mediator Which Activates Host Response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 SKPIDASRLDLRIGCIVTAKKHPDADSLYVEEVDVGEAAPRTVVSGLVNHVPLEQMQNRM 60
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Pred. No. 3.9e-69;
6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 KKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQTMSNSGIK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: 1BM PC_compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.30, Version #1.30
CURRENT APPLICATION DATA:
FPLICATION NUMBER: US/09/851,026
FILING DATE: 07-May-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Famodu, Layo O.
APPLICANT: Antoni Rafalski
TITLE OF INVENTION: Methionine Metabolic Enzymes
FILE REFERENCE: BB-1241
CURRENT APPLICATION NUMBER: US/09/392,772
CURRENT FILING DATE: 1999-09-07
BARLIER APPLICATION NUMBER: 60/099,519
EARLIER FILING DATE: 1998-09-08
NUMBER OF SEQ 1D NOS: 12
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: White, John P.
REGISTRATION WUMBER: 28,678
RERERENCE/DOCKET NUMBER: 41735-A-PCT-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/360,821
FILING DATE: 08-OCT-96
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: Peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-051-026-11
                                                                                                                                                                                                                                                                                                                                                 ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/09392772
Patent No. 6346403
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 166 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 212-278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.1%;
                                                                                                                          NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                              CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 94.0
Matches 156; Conservative
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                                                                                                                              Sequence 11. Application US/08360821B
Sequence 11. Application US/08360821B
Patent No. 6228837
GENERAL INFORMATION:
APPLICANT: Stear, Matthias
APPLICANT: Kay and M.
APPLICANT: Kay and M.
APPLICANT: Kay and M.
APPLICANT: Kay and M.
APPLICANT: Matthias
APPLICANT: Matthias
APPLICANT: Matthias
APPLICANT: Matthias
APPLICANT: Interest Matthias
APPLICANT: Matthias
APPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 VILLCNLKPAKMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAFPGEPDKELNP 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SKPIDASRLDLRIGCIVTAKKHPDADSLYVEEVDVGEAAPRTVVSGLVNHVPLEQMQNRM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53.1%; Score 835; DB 3; Length 166; 94.0%; Pred. No. 3.9e-69; Live 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 KKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQTMSNSGIK 312
121 KKKIWEQIQPDLHTNAECVATYKGAPFEVKGKGVCRAQTMANSGIK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: C.C. COMPUTER READABLE FORM:

ZIP: 10036

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.30, Version #1.30

CURENT APPLICATION NUMBER: US/08/360,821B

FILING DATE: 08-OCT-96

CLASSIFICATION: 435

ATTORNEY/AGRT INPORMATION:

NAME: White, John P. REGIESTRATION NUMBER: 28,678

REGIESTRATION NUMBER: 28,678

REGIESTRATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAK: 212-391-0525

TELEFAK: 212-391-0525
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Patent No. 6734168
GENERAL INFORMATION:
APPLICANT: Stern, David M.
Clausg, Matthias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 94.0
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: New York
STATE: New York
COUNTRY: USA
                                                                                               RESULT 12
US-08-360-821B-11
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US-09-851-026-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTK--EQIKGGTGD 119
                                                                                                                                                                                                                                                                                                               430 LKDE------DVALHREKYAGSQAERSSKAAADAEANKVANQLKG---- 468
                                                                                                                                                                                                                                                                                                                                                        120 EKKAKEKIEKKGEKKEKKQQSIAGSADSK----PIDVSRLDLRIGCIITARKHPDADSLY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                   176 VEEVDVGEIAPRIVVSGLVNHVPLEOMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPE- 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 -KIEILAPPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPF 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63;
                                                                                                                    DB 3; Length 659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          '; Sequence 1, Application US/08705868
; Patent No. 5885798
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Coleman, Roger
; APPLICANT: Au-Young, Janice
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: NOVEL MONOCYTE ACTIVATING CYTOKINE
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
                                                                                                                  Query Match
32.5%; Score 510.5; DB 3; Length 6
Best Local Similarity 38.6%; Pred. No. 2.3e-38;
Matches 123; Conservative 49; Mismatches 84; Indels
                                                                                                                                                                                               18 ADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTY: U.S.

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FasteSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,868
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0117 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    642 TTSA-GVCRVKTIANGEIR 659
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 301 amino acide
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3174 Port
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
                                TYPE: PRT

CRGANISM: Zea mays
US-09-392-772-10
                    LENGTH: 659
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US-08-705-868-1
SEQ ID NO 10
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165 IDVGEARPRIVVSGLVQFVPKEELQDRLVVVLCNLKPQKMRGVESQGMLLCASIEGINRQ 224
                                                                                                                                                                                                    123 AKEKIEKKGEKKEKKQQSIA-GSA-DSKPIDV--SRLDLRIGCIITARKHPDADSLYVEE 178
                                                                                                                                                                                                                      179 VDVGEIAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSP---EK 235
                                                                                                                                                                <u>ئ</u>
                                                                                                                          Length 301;
                                                                                                                                                                51; Indels
                                                                                                                        ch 28.0%; Score 440.5; DB 2;
1 Similarity 49.5%; Pred. No. 2e-32;
94; Conservative 36; Mismatches 51;
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he : 43 secs
             MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
                                                                                                                                                                                                                                                                                                                                                                                                                           295 VK-GKGVCRA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                             285 TKLGSISČKS 294
TOPOLOGY: linear
                                                                                                                            Query Match
Best Local Similarity
Matches 94; Conserv
                                                                                       US-08-705-868-1
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Sequence 6, Appli Sequence 6, Appli Sequence 2, Appli Sequence 157861, Sequence 197042, Sequence 197042, Sequence 33595, Sequence 31897, Sequence 340858, Sequence 41506, Sequence 240858, Sequence 240858, Sequence 240858, Sequence 25354,

Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 304067,

US-10-240-5232-22 US-10-240-527A-22 US-10-425-115-304067 US-10-425-115-197045 US-10-424-599-157860

Sequence 197045, Sequence 157860,

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Result Š.

Sequence 2, Appli Sequence 2, Appli Sequence 372, App Sequence 132, App

6 US-10-425-115-350232 6 US-10-437-931-183001 US-10-823-730-2 6 US-10-425-116-350231 5 US-10-425-114-37579 6 US-10-425-116-350231 6 US-10-425-116-350231 6 US-10-425-118-3 10 US-09-813-118-2 6 US-10-240-532-2 6 US-10-240-532-6 6 US-10-30-813-718-6 10 US-09-813-718-6 10 US-09-813-718-6 10 US-09-813-718-6 10 US-09-813-718-6 10 US-09-813-718-6 10 US-10-440-8532-15-861 10 US-10-445-115-357897 10 US-10-425-115-361131 10 US-10-425-115-36131 10 US-10-425-115-3613346 10 US-10-425-115-36349

Sequence:

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Searched:

Database

Sequence 183003, Sequence 37579, A Sequence 350211, Sequence 2, Appli

Sequence

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1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
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Sequencial INFORMATION:

PUBLICATION NO. US20050069886A1

GENERAL INFORMATION:

APPLICANT:

FILE REFERENCE:

CURRENT PELICATION NUMBER:

CURRENT FILING DATE: 2004-05-07

PRIOR APPLICATION NUMBER: 60/331,042

PRIOR APPLICATION NUMBER: 60/331,041

PRIOR PILING DATE: 2001-11-07

PRIOR PILING DATE: 2001-11-07

PRIOR FILING DATE: 2001-11-18

PRIOR FILING DATE: 2001-07

NUMBER OF SEQ ID NOS: 52

SOFTWARE: PATENTING DATE: 2001-07

SEQ ID NO 97

FENOTTALING DATE: 2001-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                               227.4
227.3
225.2
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223.0
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430.5
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407.5
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Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 36, Appl
Sequence 35, Appl
Sequence 7, Appli
Sequence 11, Appl
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                                                                                                                                         (without alignments)
764.514 Million cell updates/sec
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                                                                                                                                                                                                                           1 MANNDAVLKRLEOKGAEADQ.....FEVKGKGVCRAQTMSNSGIK 312
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17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
                                                                                                                   August 3, 2005, 21:51:44 ; Search time 159 Seconds
                GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 US-10-494-940-47

7 US-10-623-567A-1

US-09-851-026-36

US-09-851-026-36

US-09-851-026-37

US-09-851-026-11

US-09-930-169-3

6 US-10-823-730-3

6 US-10-823-730-1

6 US-10-823-730-1

6 US-10-823-730-1

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                                                                                                                                                                                                                                                                                                                   1745140 segs, 389608008 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
                                  Copyright
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999.7
885.7
600.5
533.1
522.8
523.8
455.1
33.6
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1568
1343
1343
951
831
831
709
709
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Kao, cance
Kayton, Mark
Libutti, Steven K
TITLE OF INVENTION: Endothelial Monocyte Activating
Polypeptide II: A Mediator Which Activates Host Response
                                                                                                                                                                                                                                                                                                                                  ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/360,821
FILING DATE: 08-007-96
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                             ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/09/851,026
FILING DATE: 07-May-2001
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acide
STRANDEDNESS: single
STRANDEDNESS: single
TOPOLCGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-09-851-026-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 312 amino acids
  GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Stern, David M.
Clauss, Matthias
Kao, Janet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 36
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                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
Patent No. US20020160957A1
                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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                            KKAKEKIEKKGEKKEKKQOSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVD 180
                                                                                                                                                                                           181 VGEIAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKNRGVLSQAMVMCASSPEKIEILA 240
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                                                                                                                                                                   VGEIAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/10621567A; Sequence 1, Application Wo. US20050119175A1; Publication No. US20050119175A1; Publication No. US20050119175A1; Publication No. US20050119175A1; Publication No. US20050119175A1; APPLICANT: Kim, Sunghoon; TITLE OF INVENTION: Method for Stimulating Wound Healing; FILE REFERENCE: 012679-093; CURRENT APPLICATION NUMBER: US/10/623,567A; CURRENT FILING DATE: 2003-07-22; PRIOR PILING DATE: 2002-07-22; NUMBER OF SEQ ID NOS: 7; SOFTWARE: PastSEQ for Windows Version 4.0; SEQ ID NO 1; ENGTH: 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 1573; DB 17;
100.0%; Pred. No. 1.2e-118;
tive 0; Mismatches 0;
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j Sequence 36, Application US/09851026
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Matches 312; Conservative
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ORGANISM: Homo sapiens
US-10-623-567A-1
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                                                                                                                                                                                                  61 ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
                                                                                                                                1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE 60
                                                                                                                                                                                                                                                                                                                                                                                                                           181 VGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA
                                                                                                  1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
                                                    Gaps
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Length 312;
                                                    Indels
Ouery Match
99.7%; Score 1568; DB 9;
Best Local Similarity 99.7%; Pred. No. 3e-118;
Matches 311; Conservative 0; Mismatches 1;
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Sequence 10. Application US/09851026
Sequence 10. Application US/09851026
Patent No. US20020160957A1
GENERAL INFORMATION:
APPLICANT: Starthias
Kao, Janet
Kayton, Mart
Kayton, Mark
Libuti, Steven K
IIDLE OF INVENTION: Endothelial Monocyte Activating
Polypeptide II: A Mediator Which Activates Host Response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIBILAPPNGSVPGD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 RITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQTMSNS 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNAECVATYKGAPFEVKGKG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                        Sequence 7, Application US/10910403
; Sequence 7, Application US/20050048616A1
; Publication No. US20050048616A1
; GENERAL INPORMATION:
    APPLICANT: Coleman et al.
; TITLE OF INVENTION: Endothelial Monocyte Activating Polypeptide III
; FILE REFERENCE: PF206D1
; CURRENT APPLICATION NUMBER: US/10/910,403
; CURRENT FILING DATE: 1997-11.18
; PRIOR APPLICATION NUMBER: US/08/972,301
; PRIOR APPLICATION NUMBER: US/08/483,534
; PRIOR APPLICATION NUMBER: US/08/483,534
; NUMBER OF SEQ ID NOS: 1997-60-7
; SOFTWARE: PatentIn version 3.0
; SSQ ID NOS: 20070072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 KGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTV
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60.5%; Sco...
100.0%; Pred. No....
0; Mismatches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                       ||||||||:|||||
298 VCRAQTMANSGIK 310
                                                300 VCRAQTMSNSGIK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 183; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Homo sapiens
US-10-910-403-7
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US-09-851-026-11
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                                                                                          Sequence 35, Application US/09851026
Patent No. US20020160957A1
GENERAL INFORMATION:
APPLICANT: Stern, David M.
Clauss, Matthias
Kao, Janet
Kayton, Mark
TITLE OF INVENTION: Endothelial Monocyte Activating
Polypeptide II: A Mediator Which Activates Host Response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVGELAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPARMRGVLSQAMVMCASSPEKIEIL 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,026
FILING DATE: 07-MAy-2001
CLASSIFICATION: 4UNknown>
PRIOR APPLICATION NUMBER: US/08/360,821
FILING DATE: 08-OCT-96
ATTORNEY/ACENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REPEREBRUCE/DOCKET NUMBER: 41735-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 35:
SEQUENCE GHARACTERISTICS:
SEQUENCE GHARACTERISTICS:
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85.9%; Pred. No. 4.5e-100;
tive 13; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham, LLP
STREET: 1185 Avenue of the Americas
CIIY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 310 amino acids
LENGTH: 310 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US-09-851-026-35
                                                                                                                                                                                                                                                                                                             SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.9*
Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10036
                                                                           -09-851-026-35
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US-09-930-169-1

Sequence 1, Application US/09930169

Sequence 1, Application US/09930169

Sequence 1, Application No. US20030004309A1

GENERAL INFORMATION:

APPLICANT: KIM, SUNGHOON

APPLICANT: KIM, SUNGHOON

TITLE OF INVENTION: HWINOLOGICAL ENHANCEMENT AGENT COMPRISING N-TERMINAL PEPTIDE OF

TITLE OF INVENTION: P43 AS AN EFFECTIVE COMPONENT

TITLE OF INVENTION: P43 AS AN EFFECTIVE COMPONENT

TITLE OF INVENTION: P43 AS AN EFFECTIVE COMPONENT

TITLE OF INVENTION: P43 AS AN EFFECTIVE

CURRENT APPLICATION NUMBER: US/09/930,169

CURRENT FILING DATE: 2001-08-16

PRIOR FILING DATE: 2001-08-16

PRIOR FILING DATE: 2001-08-16

SOFTWARE: PATENTING PATE: 2001-08-16
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/10823730

Publication No. US20040185060A1

Publication No. US20040185060A1

RENERAL INFORMATION:
TITLE OF INVENTION: Immunological enhancement agent comprising N-terminal peptide of TITLE OF INVENTION: p43 as an effective component
TITLE OF INVENTION: p43 as an effective component
FILE REFERENCE: NPF1918

CURRENT APPLICATION NUMBER: US/10/823,730

CURRENT FILING DATE: 2004-04-14

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Kopatentin 1.71

LENGTH: 166

TYPE: PRT
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                                                                                                                           61 DVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               151 DVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILL 210
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   91 MVSENVIQSTAVTTVSSGTKEQIKGGTGDEKKAKEKIEKKGEKKEKKQQSIAGSADSKPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MVSENVIQSTAVTTVSSGTKEQIKGGTGDEKKAKEKIEKKGEKKEKKQQSIAGSADSKPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNLKPAKWRGVLSQAWYMCASSPEKIEILAPPNGSVPGDRITFDAF 166
                                                                                                                                                                                                                                             CNLKPAKMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAF 256
                                                                                                                                                                                                               211 CNLKPAKMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAF 256
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Pred. No. 4.3e-59;
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100.0%; Pred. No. ...
0; Mismatches
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Best Local Similarity 100.0
Matches 166; Conservative
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US-10-823-730-3
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Publication No. US20030004309A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KIM, SUNGHOON
TITLE OF INVENTION: IMMUNOLOGICAL ENHANCEMENT AGENT COMPRISING N-TERMINAL PEPTIDE OF
TITLE OF INVENTION: IMMUNOLOGICAL ENHANCEMENT
TITLE OF INVENTION: IMMUNOLOGICAL ENHANCEMENT
FILE REFERENCE: 059333/0106
CURRENT APPLICATION NUMBER: US/09/930,169
CURRENT APPLICATION NUMBER: KR 2001-31310
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
NUMBER: OF SEQ ID NOS: 11
SOFTWARE: PARCHILIN Ver. 2.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147 SKPIDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRM 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207 VILLCNLKPAKWRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAFPGEPDKELNP 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 KKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQTMSNSGIK 312
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                                          Version #1.30
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.30, Version #
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851,026
FILING DATE: 07-May-2001
CLASSIFICATION: 'Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/360,821
FILING DATE: 08-OCT-96
ATTORNAPICATION NUMBER: US/08/360,821
FILING DATE: 08-OCT-96
ATTORNAPICATION NUMBER: 28,678
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 41735-A-PCT-US
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
TELEPHONE: 212-278-0400
TELEPHONE: 212-31-0525
INPORMATION FOR EQUI DNO: 11:
SEQUENCE CHARACTER.STICS:
LENGTH: 166 amino acids
TYBES amino acids
TYBES amino acids
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Best Local Similarity 100.0%; Pred. No. 4.3e-59;
Matches 166; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.1%; Score 835; DB 9; 94.0%; Pred. No. 2e-59; tive 6; Mismatches 4.
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TOPOLOGY: linear
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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ORGANISM: Unknown Organism
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Best Local Similarity 94.0
Matches 156; Conservative
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91 MVSENVIQSTAVTTVSSGTKEQIKGGTGDEKKAKEKIEKKGEKKEKKQQSIAGSADSKPI 150

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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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                                                                                                                                                                                                                                                                                                                                                                  235 -KIEILAPPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPF 293
                                                                                                                                                                                                                                                                                                                                                                                     276 TKVELVEPPSSAQPGERITFPGYEGNPDELLNPKKKVWETLQVDLHTNEELVACYKNVPL 335
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                                                                                                                                                             148 LKDE-----DVALHREKYAGSQAERSSKAAADAEANKVANQLKG----
                                                                                                                                     56 KKEIEELKOELIQAEIQNGVKOIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKG
                                                                                                                                                                                                                                                                                           176 VEEVDVGEIAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPE-
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                                                              Length 353;
                                                                                                  Indels
; OTHER INFORMATION: Clone ID: PAT_MRT3847_133912C.1.pep
US-10-424-599-180396
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                                                            Query Match 33.6%; Score 528; DB 15; Best Local Similarity 43.6%; Pred. No. 3.5e-34; Matches 113; Conservative 41; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: Clone ID: MRT4577_82583C.1.pep
US-10-425-115-350232
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OTHER INFORMATION: unsure at all Xaa locations
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; Sequence 350232, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 TTSA-GVCKVSSISCGSIR 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                294 EVKGKGVCRAQTMSNSGIK 312
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ORGANISM: Zea mays
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Publication. No. US20040185060A1
GENERAL INFORMATION:
APPLICANT: IMAGENE CO., LTD.
TITLE OF INVENTION: Immunological enhancement agent comprising N-terminal peptide of TITLE OF INVENTION: p43 as an effective component
FILE REFERENCE: NPF1918
CURRENT APPLICATION NUMBER: US/10/823,730
KUMBER OF SEQ ID NOS: 11
SOFTWARE: Kopatentin 1.71
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 180396, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: AND YINUA
APPLICANT: Calou Yinua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 180396
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                                                                                                                                                           ELKQELIQAEIQNGVKQIAPPSGTPLHANSMYSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
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           45.1%; Score 709; DB 10; Length 147; 100.0%; Pred. No. 2.6e-49;
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                                               Indels
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100.0%; Pred. No. 2.6e-49;
iive 0; Mismatches 0;
                       100.0%; Prec. ...
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Matches 147; Conservative
                             Best Local Similarity 100.
Matches 147; Conservative
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ORGANISM: Glycine max
PEATURE:
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ORGANISM: mammalian
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US-10-424-599-180396
                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-10-823-730-1
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Sequence 2, Application US/10823730
Publication No. US20040185060A1
GENERAL INFORMATION:
APPLICANT: IMAGENE CO., LTD.
TITLE OF INVENTION: p43 as an effective component
CURRENT APPLICATION UNMBER: US/10/823,730
CURRENT FILING DATE: 2004-04-14
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 2
LENGTH: 108
       TITLE OF INVENTION: INVENTION: INVENTION: P43 AS AN EFFECTIVE COMPONENT
TITLE OF INVENTION: P43 AS AN EFFECTIVE COMPONENT
FILE REPERENCE: 0893370106
CURRENT APPLICATION NUMBER: US/09/930,169
CURRENT PILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: KR 2001-31310
PRIOR APPLICATION NUMBER: KR 2001-31310
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKEIE
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                                                                                                                                                                                                                                                                                                                     PEATURE:
OTHER INFORMATION: Description of Unknown Organism: Mammalian
OTHER INFORMATION: protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.8%; Score 516; DB 16; Length 108; Best Local Similarity 100.0%; Pred. No. 6.5e-34; Matches 108; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 32.8%; Score 516; DB 10; Length 108; Best Local Similarity 100.0%; Pred. No. 6.5e-34; Matches 108; Conservative 0; Mismatches 0; Indels
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Job time : 161 secs
                                                                                                                                                                                                                                                                                                      ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: mammalian
                                                                                                                                                                                                                              SEQ ID NO 2
LENGIH: 108
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US-10-823-730-2
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Sequence 183001, Application US/10437963

Sequence 183001, Application US/10437963

Sequence 183001, Application US/10437963

Sequence 183001, Application US/104373434

Sequence La Rosa, Thomas J.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Bukharov, Andrey A.

APPLICANT: Branch Barbark, Bard

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REPERENCE: 38-21(51221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT PRING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 183001

LENGTH: 804
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 VPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQT 305
                                           235 -KIEILAPPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPF 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 EKKEKKQQSIAGSADSK----PIDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPR 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.9%; Score 517; DB 16; Length 804; 38.1%; Pred. No. 8.4e-33; tive 53; Mismatches 79; Indels 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_80132C.1.pep
US-10-437-963-183001
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GENERAL INFORMATION: APPLICANT KIM, SUNGHOON
                                                                                                                                       294 EVKGKGVCRAQTMSNSGIK 312
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360 TTSA-GICKVKTIANGEIR 377
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Best Local Similarity 38.17
Matches 117; Conservative
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                                                                  61 ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSG 108
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

August 3, 2005, 21:45:34 ; Search time 174 Seconds Run on:

(without alignments) 918.211 Million cell updates/sec

US-10-623-567A-1

1573

1 MANNDAVLKRLEQKGAEADQ........FEVKGKGVCRAQTMSNSGIK 312 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1612378 segs, 512079187 residues Searched: 1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q12904 homo sapien	O54873 cricetulus	P31230 mus musculu	Q8c2u7 mus musculu	Q7zwy7 xenopus lae		-					Q6tgs6 brachydanio	Q6dfz7 brachydanio	Q29465 bos taurus	P54577 homo sapien		-		Q7zx51 xenopus lae	Q6dij1 xenopus tro				Q6cki6 kluyveromyc				Q7xjm9 arabidopsis		œ	Chong ratting noun
SUPERKLES	ΩI	MCA1 HUMAN	MCA1 CRIGR	MCA1 MOUSE	Q8C2 <u>U</u> 7	Q7 ZWY7	Q9V504	070857	SYM CABEL	SYM_ORYSA	062542	SYM ARATH	QeTGS6	Q6DFZ7	SYYC BOVIN	SYYC HUMAN	SYYC_MOUSE	Q6BY38	Q9P6K7	Q72X51		G4P1 YEAST	Q6 FNN0	Q754V3	Q6CK16	QBRUPB	Q6C763	Q93VB0	6MLX7Q	09VV6Q	Q7XVQ8	6770400
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de	Query Match	100.0	96.6	85.4	85.1	68.9	42.7	39.8	S	32.9	31.8	31.7	28.8	28.7	28.6	28.6	28.4	28.1	28.1	28.0	27.9	27.3	27.1	26.9	26.4	25.6	25.5	25.5	25.5	ď.	24.9	7 7
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Q78ac3 neurospora Q9mlx8 arabidopsis O97487 euplotes oc Q7d48 anopheles g Q81148 plasmodium Q7rka7 plasmodium Q7rka7 plasmodium Q7rka7 plasmodium Q7rka7 plasmodium Q8u21 pyrococcus Q8v011 pyrococcus Q9v011 pyrococcus Q8v011 pyrococcus Q8v011 pyrococcus Q9v011 pyrococcus Q9v011 pyrococcus Q73nt9 treponema d Q73nt9 treponema d
Q7SAC3 Q9M1X8 Q9M1X8 Q07QB9 Q7QD89 Q8L148 Q7RKA7 SYM PYRFU SYM PYRAD SYM PYRAD Q72AE2 Q73M19
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419 2419 2413 4411 4402 402 403 403 403 665 665 618
22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
378.5 343.3 337.5 318.5 292.5 292.5 231.5 223.5 223.5 209.5
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

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TISSUE=Pancreas;

WEDLINE=22380825; PubMed=12477932; DOI=10.1073/pnas.242603899;

KETAURE-22380825; PubMed=12477932; DOI=10.1073/pnas.242603899;

KIGURE-22380825; PubMed=12477932; DOI=10.1073/pnas.242603899;

KIGURE-22380825; Peingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeberg B., Buetow K.H.; Scheefer C.F., Bhate N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

And Jatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

And Stapleton M.J., Usdin T.B., Forenido M.F., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.H., Rubik S.M.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahassiey N., Helton E., Ketteman M., Madan A., Rodrigues S., Banchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y. Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J.W., Schmutz J., Myers R.M.,

Rotterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
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                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=95101290; PubMed=7929199;
MEDLINE=951014290; PubMed=7929199;
Kao J., Houck K., Fan Y., Haehnel I., Libutti S.K., Kayton M.L.,
Grikscheit T., Chabot J., Nowygrod R., Greenberg S., Kuang W.J.,
Leung D.W., Hayward J.R., Kisial W., Heath M., Brett J., Stern D.M.;
"Characterization of a novel tumor-derived cytokine. Endothelial-
monocyte activating polypeptide II.";
J. Biol. Chem. 269:25106-25119(1994).
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                  012904; 036CQ9;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 45, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Multisynthetase complex auxiliary component p43 (Contains:
Endothelial-monocyte activating polypeptide II (EMAP-II) (Small
inducible cytokine subfamily E member 1)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1 tRNA-binding domain.
312 A.A.
  PRT;
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  STANDARD;
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                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
  MCA1 HUMAN
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1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE
                                                                                                                                                                                                              Name=SCYE1;
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                                                                          GO, GO:0005615; C:extracellular space; TAS.
GO; GO:000525; F:cytokine activity; TAS.
GO; GO:000649; F:rENA binding; TAS.
GO; GO:000695; P:chemctaxis; TAS.
GO; GO:0006954; P:inflammatory response; TAS.
GO; GO:0006918; P:rENA aminoacylation for protein translation; TAS.
InterPro; IPR00892; EMAPII.
InterPro; IPR008994; Nucleic_acid_OB.
InterPro; IPR002547; tRNA bind.
Fram, PF01588; tRNA bind.
PINSF; PIRSF005381; EMAPII; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 312;
                                                                                                                                                                        Endothelial-monocyte activating
polypeptide II.
FRNA-binding.
A -> P (in Ref. 2).
                                                                                                                                                      3D-structure; Cytokine; Protein biosynthesis; RNA-binding;
tRNA-binding.
PROPEP 1 146
                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1573; DB 1; Length 100.0%; Pred. No. 4e-83; cive 0; Mismatches 0; Indels
 Usage by
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 modified and this statement is not removed.
       entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
                        EMBL; U10117; AAA62202.1; -. EMBL; BC014051; AAH14051.1; -. PDB; 1E72; X-ray; A=147-312. PDB; 1EUU; X-ray; A+B=47-312. PDB; 1FL0; X-ray; A=150-312. Genew; HGNC:10648; SCYE1. H-INVB; HX0004426; -.
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312 AA;
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Best Local Similarity
Matches 312; Conserv
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                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                           PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV 300
                                      121 KKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98070438; PubMed=9405472; DOI=10.1074/jbc.272.51.32573; MEDLINE-98070438; PubMed=9405472; DOI=10.1074/jbc.272.51.32573; MEDLINE-98070438; PubMed=9405472; DOI=10.1074/jbc.272.51.32573; Quevillon S., Agou F., Robinson J.-C., Mirande M.; The p43 component of the mammalian multi-synthetase complex is likely to be the precursor of the endothelial monocyte-activating polypeptide II cytokine."; J. Biol. Chem. 272:32573-32579(1997).

- SUBGNIT: Component of the multisynthetase complex which is comprised of a bifunctional glutamyl-prolyl-tRNA synthetase, the monospecific isolencyl, leucyl, glutaminyl, methionyl, lysyl, arginyl, and aspartyl-tRNA synthetases as well as three auxiliary proteins, p18, p48 and p43.

- SIMILARITY: Contains 1 tRNA-binding domain.
                                                                                                                                                                                                                                                                                                                                  VGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILA
                                                                                                                                                                                                                                                                                                                                                                        ELKOELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Multisynthetase complex auxiliary component p43 [Contains:
Endothelial-monocyte activating polypeptide II (EMAP-II) (Small inducible cytokine subfamily E member 1)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; 1PR00823; EMAPII.
InterPro; IPR008994; Nucleic acid_OB.
InterPro; IPR002847; FRNA_bind.
Pfam; PF01898; trNA_bind; 1.
PIRSF005381; EMAPII; 1.
PROSITE; PS50886; TRBD; 1.
Cytokine; Protein biosynthesis; RNA-binding; tRNA-binding.
1 194 By similarity.
CHAIN 194 S59 Endothelial-monocyte activating
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Eukaryota, Metazoa, Chordata, Crania
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altasner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worlby K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Villalon D.K., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
                                                                                                                                                                                                      226 VDVGEAAPRTVISGLVNHVPLDQMQNRWVLLCNLKPAKMRGILSQAMVMCASSPEKVEI 285
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                                                                                                                                                                              1 MANNDAVLKRLEGKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILINE-55014290; PubMed=7929199; Kabutti S.K., Kayton M.L., Kao J., Houck K., Fan Y., Haehnel I., Libutti S.K., Kayton M.L., Grikacheit T., Chabot J., Nowygrod R., Greenberg S., Kuang W.J., Leung D.W., Hayward J.R., Kisiel W., Heath M., Brett J., Stern D.M.; "Characterization of a novel tumor-derived cytokine. Endothelial-monocyte activating polypeptide II.";
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Sciurognathi, Muridae, Murinae, Mus.
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Endothelial-monocyte activating polypeptide II (EMAP-II) (Small
inducible cytokine subfamily E member 1)].
                                                                                   86.6%; Score 1362.5; DB 1; Length 359; 86.0%; Pred. No. 6.4e-71; ive 19; Mismatches 22; Indels 3;
                    RNA-binding.
4D868D1B65D72C23 CRC64;
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polypeptide II.
                         LRNA
                                            39601 MW;
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Mammalia, Eutheria, Rodentia,
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                                                                                                                                    Matches 270; Conservative
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                         198 2
359 AA;
                                                                                                               Similarity
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
                                                                                                                                                                                                              SEQUENCE OF 145-164 FROM N.A. MEDILIBE-39315897; Pubmede-1400342; MEDILIBE-39315897; Pubmede-1400342; Kao J., Ryan J., Brett G., Chen J., Shen H., Fan Y.-G., Godman G., Familletti P.C., Wang F., Pan Y.-C.E., Stern D., Clauss M.; Endchellal monocyte-activating polypeptide II. A novel tumor-derived polypeptide that activates host-response mechanisms."; J. Biol. Chem. 267:20239-20247(1992).
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PROSITE; PS50886; TRBD; 1.
Cytokine; Protein biosynthesis; RNA-binding; tRNA-binding.
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                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Pred. No. 7.3e-70;
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tRNA-binding.
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85.9%; Pred. No. 7.3e-
tive 13; Mismatches
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MGD, MGI:102774, SCYP1.
InterPro; IPRO08232; EMAPII.
InterPro; IPRO08994; Nucleic acid OB.
InterPro; IPRO08994; Nucleic acid OB.
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EMAPII; 1.
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Genome Res. 10:1757-1771 (2000)
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TISSUE=Embryo;
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                                                                                                                                               240 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKG 299
                                                                                                                                                                          EKKVKEKTEKKGEKKE-KQQSAAASTDSKPIDASRLDLRIGCIVTAKKHPDADSLYVEEV 177
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
length enriched library, clone:B43001B22 product:endothelial monocyte
activating polypeptide 2, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=NOD; TISSUE=Thymus; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation 60,770 full-length cDNAs."; Nature 420:563-673 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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STRAIN=NOD; TISSUE=Thymus;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                319 AA.
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The FANTOM Consortium,
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STRAIN=NOD; TISSUE=Thymus;
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Addchi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Karoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saico R., Saico H., Sakai C., Sakai K., Shiraki T., Sogabe Y., Tagami M., A Sasaki D., Shibata K., Shinagawa A., Firzki T., Sogabe Y., Tagami M., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Tamaka T., Shiraki A., Muramatsu M., Hayashizaki Y., Embi. AKOR 7922; BAC 40045.1; -.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 85.1%; Score 1338; DB 2; Length 319; Best Local Similarity 85.3%; Pred. No. 1.5e-69; Matches 267; Conservative 15; Mismatches 27; Indels
multicapillary sequencer.";
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Last annotation update)
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G0; G0:0003576; F:nucleic acid binding; IEA.
G0; G0:0000049; F:RNA binding; IEA.
InterPro; IPR008994; Nucleic acid OB.
InterPro; IPR008994; Nucleic acid OB.
Feam; PF01588; tRNA bind.
PROSITE; PS50886; TRNA, bind.
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Xenopus laevis (African clawed frog)
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01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
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OD; TISSUE=Thymus;
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MEDLINE=22426070; PubMed=12537573;
293 AR 294
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          Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Boatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
Generation and initial analysis of more than 15,000 full-length human
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MEDIINE=22341112; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                     'Genetic and genomic tools for Xenopus research: The NIH Xenopus
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 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC046580; AAH46580.1; -.
HSSP; Q12904; 1FL0.
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GO; GO:0000049; F:tRNA binding; IEA.
INTERPRO! SPRO08932; EMAPII.
INTERPRO! IPR008994; Nucleic acid_OB.
INTERPRO! IPR002547; TRNA_bind.
PHAR; PROSESF; EMAPI!; 1.
PROSITE; PS50886; TRBD; 1.
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REDEINNE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

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Sutcon G.G., Wortnan J.R., Yandell M.D., Zhang O., Chen L.K.,

RADAGEN R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeitfer B.D.,

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Borkova D., Botchen M.R., Bouck J., Rokstein P., Brottier P.,

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RADAGEN R., Worker R., Vannison M., Strong R., Sun E.,

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RADAGEN R., Worker R., Weinsenbach J.,

RADAGEN R., Worker R., Weinsenbach J.,

RADAGEN R., Radagen R., Rubin G.,

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                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Boptera; Endoptera; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                Last sequence update)
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323 AA
                                                                                  Created)
PRT;
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MEDLINE=22426065; PubMed=12537568;
                                                                              01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2004 (TrEMBLrel. 26,
PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 LIQAEIQNGVKQIAFP----SGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAPPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGK 298
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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE=22426069; PubMed=12537572;

Mista S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.

Bettencourt B.R., Celniker S.E., de Grey A.D., Drydale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                    'Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 AA; 34401 MW; 6EEB6E30115F4E84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.7%; Score 671; DB 2;
44.9%; Pred. No. 4.4e-31;
tive 57; Mismatches 88;
                                                                                              a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HESPS; Q12094; IEUJ.

INCACT; Q9V504;

FlyBase; PEGN03331; CG8235.

G0; G0:0003676; F:nucleic acid binding; IEA.

G0; G0:000049; F:ENA binding; IEA.

INCEPTO: IPR008232; EMAPII.

INCEPTO: IPR008994; Nucleic acid OB.

INCEPTO: IPR008994; Nucleic acid OB.

PEGN; PF01589; ENAPII.

PIRSF; PIRSF005381; EMAPII; 1.

PROSITE; PS50886; TRBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE003835; AAF59019.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVCRAQTMSNSGIK 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 44.9
Matches 141; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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351 AA

PRT;

PRELIMINARY;

RESULT 7 Q7Q8S7 ID Q7Q8S7

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238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 LAPPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 SLEVAHĞKVÖİPVPTPDEVRAĞSGPATVKMEPVAĞPPA---AKESPKEĞPPAKAQQKQSD 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 EKKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 LKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEIEELKQELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 QAEIQNGVKQIAFPSGTPLHANS----MVSENVIQSTAVTTVSSGTKEQ----IKGGTGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVGE-IAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                       Anopheles gambiae str. PEST.
Bukaryota, Metaroa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=180454;
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Methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                       Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL; AAAB01008933; EAA09959.1; --
HSSP; Q12904; 1EUJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 AA; 38153 MW; F3F1E2D23B1E3DFE CRC64;
01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
AgCP11872 (Fragment).
Name=agCG47516, ORFNames=EMSANGG0000014444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.8%; Score 625.5; DB 2; 42.7%; Pred. No. 2e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; Q12904; IEUJ.
GO; GO: 0003676; F: nucleic acid binding; IEA.
GO; GO: 0000049; F: FRNA binding; IEA.
INCEPPO; IPR008932; EMAPII.
INCEPPO; IPR00894; Nucleic acid OB.
INCEPPO; IPR002847; tRNA bind.
PF01589; tRNA bind.
PRSF; PREF005381; EMAPII; 1.
PROSITE; PS50866; TRBD; 1.
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Matches 134; Conservative 53; Mismatches
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15-DEC-1998 (Rel. 37, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=mrs-1; ORFNames=F58B3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 GVCRAQTMSNSGIK 312
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GPVKAQTLKNVQVK 351
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                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                 STRAIN=PEST;
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839 DKVEIMEVPADSKPGTPVVCPPYTHRPDEQLNPKKKIWETVAEDLKVSAEGFAEWKGQPL 898
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PEAM; PF00133; FRNA-synt 1; 1.
PIRSP; PIRSPO01528; MerRS dimerising; 1.
PRINTS; PR01041; TRNASYNTHMET.
PROFIME; PF00198; metG; 1.
PROSITE; PF00178; AA TRNA_LIGASE 1; 1.
PROSITE; PF00186; TRBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR008224; MetRS dimerising
InterPro; IPR008994; NucleTc acid OB.
InterPro; IPR002300; tRNA-8ynt_la.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002300; t.m....r. InterPro; IRR001412; tRNA-synt I. InterPro; IPR002304; tRNA-synt met. InterPro; IPR002547; tRNA-bind. InterPro; IPR09080; tRNASyn la-bind.
                                                                                                                                                                                                     PRT;
                                                294 EVKGKGVCRAQTMSNSGIK 312
                                                                                          917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF040700; AAC99620.1; -.
                                                                                          899 LIGSESKMTAPTLRGVHVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA-binding, tRNA-binding DOMAIN 4 11
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                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         804 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gramene; Q9ZTS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sest Local Simi
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ID SYM O
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                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP: 012904; 14299; 142899; 142899; 142899; 142899; 142899; 142899; 142899; 142899; 142899; 142899; 142899; 142899; 142899; 15808324; MetRS dimeriaing.

R InterPro; 1FR006324; MetRS dimeriaing.

R InterPro; 1FR006394; Nucleic_acid_0B.

R InterPro; 1FR002300; ERNA-synt_la.

R InterPro; 1FR002304; ERNA-synt_met.

R InterPro; 1FR002304; ERNA-synt_met.

R InterPro; 1FR002304; ERNA-synt_li.

R InterPro; 1FR002980; ERNA-synt_li.

R Pfam; PF00133; ERNA-bind; 1.

P RSSP001285; ERNA-bind; 1.

R PRINTS; PRSF001285; MetRS dimeriaing; 1.

R PRINTS; PRS0014; TRNASYNTHMET.

R PROSITE; PS00178; AA TRNA_LIGASE_I; 1.

R PROSITE; PS50886; TRBD; 1.

R Aminoacyl-tRNA synthetase; ATP-binding; Ligase; Protein biosynthesis; MNA-binding; LRNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  677
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSP 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 GDEKKAKEKIEKKGEKKEKKQQSIAGSADSKP----IDVSRLDLRIGCIITARKHPDADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MANNDAVLKRLEQKGAEADQII-EYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEI
                                                                                                                                                                                                                                                                           SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                        CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP diphosphate + L-methionyl-tRNA(Met).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.9%; Score 564; DB 1; Length 917; 42.3%; Pred. No. 2.1e-24;
                                                                                                                      The C. elegans sequencing consortium;
faconome sequence of the nematode C. elegans: a platform for
investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.3%; Pred. No. 2.15-27,
tive 52; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .917 AA; 101713 MW; 3B42AABA314FBDF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "KMSKS" region.
ATP (By similarity).
tRNA-binding.
                                                                                                                                                                                                                                                                                                     family.
-!- SIMILARITY: Contains 1 tRNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "HIGH" region.
                                                                          STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z73427; CAA97803.1; -. PIR; T22898; T22898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 42.3
Matches 135; Conservative
      NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174
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BINDING
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           NAME OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-OCT-2004 (Rel. 45, Last annotation update)
Probable methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA ligase) (MetRS)
                                                                                                                                                                                                                                           Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Deniziak M., Mirande M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ATLIVITY: ATP + L-methionine + tRNA(Met) = AMP +

-i- CATALYTIC ATLIVITY: ATP + L-methionine + tRNA(Met) = AMP +

-i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).

-!- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "HIGH" region.
"KMSKS" region.
ATP (By similarity).
tRNA-binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 tRNA-binding domain.
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804 AA.
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Probable methionyl-tRNA synthetase (EC 6.1.1.10) (Methionine--tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thaliana.";
276
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                                                          ------FRNKFAGSQAERSSKAQADAEAKKVADKLKG-----TKLSDGG 620
                                                                                                                                                                                      TVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPE--KIEILAPPNGS 245
                                                                                                                                                                                                                                                                       246 VPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQT 305
                                                                                                                                                                                                                                                                                               GVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTK--EQIKGGTGDEKKAKEKIEKKG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRIGRITSVERHPDADTLYVEQIDVGEEKPRTVCSGLVTHVAIETMNNRLVVVLCNLKEV 60
                                                                                                                                                                                                              MEDLINE=98184040; PubMed=9523439; DOI=10.1098/rspb.1998.0311; Pahler S., Krasko A., Schuetze J., Mueller T.M., Mueller W. B.G.; Infoolation and characterisation of the cDNA, encoding a potential morphogen from the marine sponge Geodia cydonium that is conserved in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KWRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQP
                                                                                                    EKKEKKOOSIAGSADSK----PIDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 LRIGCIITARKHPDADSLYVBEVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Endothelial-monocyte-activating polypeptide related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 AA; 16499 MW; 61272889BE17C7EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. R. Soc. Lond., B, Biol. Sci. 265:421-425(1998).

BMBL; Y14947; CAA75164.1; -.

HSSP; Q12904; FLO.

GO; GO:00003576; F:uncleic acid binding; IEA.

GO; GO:000049; F:tRNA binding; IEA.

InterPro; IPR008994; Nucleic acid_OB.

InterPro; IPR008994; Nucleic acid_OB.

Pram; PF01588; tRNA bind.

PROSITE; PSSO886; TRBD; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 AA.
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Astrophorida; Geodiidae; Geodia.
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798 IASGEIR 804
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AC 06254
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DT 01-AU DT 01-00
DT 01-00
DE Endot GN Geodii
CC AGLO
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797 AA

PRT;

STANDARD;

RESULT 11 SYM_ARATH ID SYM_ARATH

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Re Sections of From W.A.

Re Sections of From W.A.

Re Model Columbia (Columbia)

Resider (Columbia)

R
ligase) (MetRS).
OrderedLocusNames=At4gl3780; ORFNames=F18A5.170;
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Erreptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicoryledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- CATALYTIC ACTIVITY: ATP + L-methionine + tRNA(Met) = AMP + diphosphare + L-methionyl-tRNA(Met).
-i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-i- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 1 tRNA-binding domain.
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EMBL; AY398430; AAQ97863.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                    PNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUENCE FROM N.A.

TISSUE Kidney marrow;
Song H.D., Wu X.Y., Sun X.J., Zhou Y., Liu T.X., Deng M., Zhang G.W.,
Shong Y., Chen Y., Kuan Z., Jiang C.L., Fan H.Y., Zon L.I.,
Shong Y., Look A.T., Chen Z.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                  Aminoacyl-tRNA synthetase; ATP-binding; Ligase; Protein biosynthesis; RNA-binding; tRNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Tyrosyl-tRNA synthetase.
Name=yars, Synonyms=YARS,
Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                  51; Indels
                                                                                                                                                                                                                                                                                     348 352 "KMSKS" rēgion.
351 351 ATP (By similarity).
635 738 tRNA-binding.
797 AA; 89853 MW; B0F523C2E0C1017F CRC64;
                                                                                                                                                                                                                                                                                                                                            31.7%; Score 499; DB 1; 52.9%; Pred. No. 1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      529 AA
                                                                                                                                                                                                                                                                                                                                                                   31; Mismatches
                                                                                             UniterPro; 1PR008924; MetRS dimerising.
InterPro; 1PR008994; Nucleic acid OB.
InterPro; 1PR008994; Nucleic acid OB.
InterPro; 1PR001412; ENRA-synt _1.
InterPro; 1PR001412; ENRA-synt _1.
InterPro; 1PR002004; tRNA-synt _1.
InterPro; 1PR002047; tRNA-synt _1.
InterPro; 1PR002080; tRNA-synt _1.
Pfam; PF0013; tRNA-synt _1; 1.
Pfam; PF0013; tRNA-synt _1; 1.
PRSF; PRSF001528; MetRs dimerising; 1.
PRSF; PRSF001528; MetRs dimerising; 1.
TIGRRAMS; TIGR00039; metCs.
TIGRRAMS; TIGR00399; metCs.
                                                                                                                                                                                                                                                                            "HIGH" region.
           entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
 and this statement is not
                                           EMBL, AL035528; CAB36842.1; -. EMBL, AL16133; CAB78420.1; -. PIR, T05247. T05247. HSSP, Q12904; 1E72.
                                                                                                                                                                                                                                                                                                                                                                   Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVSSISNGTIR 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 RAQTMSNSGIK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                       GeneFarm; 2798;
                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 787
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                                                   BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OCTGS6
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Q6TGS6
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-KKQQSIA-----GSADSKP----IDVSRLDLRIGCIITARKHPDADSLYVEE 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393 IDVGEEQPRTVVSGLVAYITEEQLQDRLVVLLCNLKPQKMRGIBSQAMVLCASIBGEPRK 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 IEILAPPNGSVPGDRITFDAF-PGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 FGGDKVYTDFEEVEKDFAA------EQIH--PGDLKASVELALNKLLDPIRKKFESPE 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ENVIOSTAVTTVSSGTKEQIKGGTGDEK-----KAKEKIEKKGEKKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44 EEKKLRV--ENAKLKKEIEELKOELIQAEIQNG----VKQIAFPSGTPLHANSMVS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brachýdanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB=Whole;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Høleh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.8%; Score 453.5; DB 2; Length 529; Best Local Similarity 39.8%; Pred. No. 2.7e-18; Matches 123; Conservative 43; Mismatches 78; Indels 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                529 AA; 59505 MW; C3314003813B9336 CRC64;
ZFIN; ZDB-GENE-030425-2; yars.

GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003524; F:ATP binding; IEA.
GO; GO:000049; F:LRNA binding; IEA.
GO; GO:0004931; F:tyrosine-tRNA ligase activity; IEA.
GO; GO:000437; P:tyrosine-tRNA aminoacylation; IEA.
InterPro; IPR008392; EMAPII.
InterPro; IPR008394; Nucleic acid OB.
InterPro; IPR002305; tRNA-synt_1b.
InterPro; IPR002307; Tyr ENA-synt_1b.
Pfam; PF00579; tRNA-synt_1b.
Pfam; PF00579; tRNA-synt_1b.
Pfam; PF01588; tRNA-synt_1b.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                        PIRSF; PIRSF005381, EMAPI1; 1.
PRINTS; PRO1040; TRNASYNTHTYR.
TIGRPAMS; TIGR00234; LYFS; 1.
PROSITE; PSS50886; TRBD; 1.
Aminoacyl-tRNA synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tyrosyl-tRNA synthetase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 VK-GKGVCR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           513 TKLGRITCK 521
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Query Match
    -----ENVIQSTAVTTVSSGTKEQIXGGTGDEK-----KAKEKIEKKGEKKE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----KKQQSIAG----SADSKPIDVSRLDLRIGCIITARKHPDADSLYVEE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 LKKLTSSAYPEPSKNKGGVKGNPKQTTDDDEVIPSRLDIRVGKVISVEKHPDADSLYLEK 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VDVGEIAPRTVVSGLVNHVPLEOMONRMVILLCNLKPAKMRGVLSQAMVMCAS---SPEK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 FGGDKVYTDFEEVEKDFÅA-----EQIH--PGDLKASVELALNKLLDPIRKKFESPE 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236 IEILAPPNGSVPGDRITFDAF-PGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFE 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 EEKKLRV--ENAKLKKEIEELKQELIQAEIQNG----VKQIAFPSGTPLHANSMVS---- 93
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., Malek J.A., Gunaratne P.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Stalska W., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 529;
                                                                                                                                                                                                                               A Straubberg R.;
Lubmitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
Lubmitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
R GO; GO:0005524; R.APP binding; IEA.
GO; GO:000049; F:APP binding; IEA.
GO; GO:000049; F:RNA binding; IEA.
R GO; GO:000049; F:RNA binding; IEA.
R GO; GO:000493; F:LYCOS1-ENAR aminoacylation; IEA.
R InterPro; IPR008223; EMARI.
R InterPro; IPR008234; RAMA-Synt_lb.
R InterPro; IPR002305; TRNA-Synt_lb.
R InterPro; IPR002307; TRNA-Synt_lb.
R InterPro; IPR002307; TRNA-Synt_lb.
R EAM; PP01588; RRNA-Synt_lb; I.
R Fam; PR01588; RRNA-Synt_lb; I.
R FIRSF; PIRSF00539; EMARI:
R INTERPRO; IRROPASANTHIYR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.7%; Score 451.5; DB 2; Length 5: 38.5%; Pred. No. 3.5e-18; ive 46; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aminoacyl-tRNA synthetase,
SEOUENCE 529 AA; 59533 MW; A3264E3E39D362F4 CRC64;
                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                      and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 38.5
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50886; TRBD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VK-GKGVCR 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             513 TKLGRITCK 521
                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
SYYC BOVIN
ID SYYC BOVIN
AC Q29465; Q9TSJ1;
                                                                                                                                                                                                                          TISSUE=Whole;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295
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527 AA.

STANDARD;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93
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25-OCT-004 (Rel. 45, Last sequence update)
25-JAN-2004 (Rel. 46, Last sequence update)
Tyrosyl-tRNA synthetase, cytoplasmic (EC 6.1.1.1) (Tyrosyl--tRNA ligase) (TyrRS)
Name=YARS; Synonyms=TYRS;
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matsuka G.K.H., Naidenov V.G., Odynets K.A., Woodmaska M.I., Matsuka G.K.H., Wientjes F.-J., Gassen H.G., Kornelyuk A.I.; Amino acid sequence of bovine tyrosyl-tRNA synthetase. Possible generation of the isolated cytokine-like C-terminal domain via proteolytic cleavage at the 'PEST'-like sequence.";
                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diphosphate + L-tyrosyl-tRNA (Tyr).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Liver;
Kornelyuk A.I., Levanets O.V., Naidenov V.G., Woodmaska M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acetylation; Aminoacyl-tRNA synthetase; ATP-binding; Ligase; Protein biosynthesis; RNA-binding; tRNA-binding.

INIT MET 0 0 By similarity.

OND RES 1 1 N-Acetylglycine (By similarity).

SITE 221 225 "KOKSKS" region.

DOMAIN 363 467 tRNA-binding.

CONFLICT 20 V -> A (in Ref. 2).

SEQUENCE 527 AA; 59018 MW; E3F66789F75EA7D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DB 1; Length 527;
4.2e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteolytic cleavage at the 'PEST'-like sequence.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases -1- CATALYTIC ACTIVITY: ATP + L-tyrosine + tRNA(Tyr) = ^{1}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: Contains 1 tRNA-binding domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO1040; TRÑASYNTHTYR.
TIGRRAMS; TIGR00234; tyrS; 1.
PROSITE; PSO1018; AA TRNA_LIGASE_I; FALSE_NEG.
PROSITE; PSS0886; TRBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.6%; Score 450; DB
36.9%; Pred. No. 4.2e
tive 55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR008994; Nucleic_acid_OB.
InterPro; IPR002305; RNNA-synt_1b.
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002547; tRNA_bind_.
InterPro; IPR002547; tRNA_bind_.
Pfam; PF00579; tRNA-synt_lb, 1.
Pfam; PF00589; tRNA-synt_lb, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF087021; AAC82467.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 16-211 FROM N.A.
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Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                 Bovinae; Bos
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THE MENT TO BE A SECTION OF THE SECT
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WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETAUSDERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIJAUSDERG R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RIJAUSDERG R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Robert B., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rable S.A., Loquellano N.A., Peterg G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Robert S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiting M., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Schalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Shalska U., Smailus D.E.,

Conforcation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                     132 EKK-----EKKQQSIAGSA-DSKPIDV--SRLDLRIGCIITARKHPDADSLYVEEV 179
                                                                                                                                                                                                      DVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSP---EKI 236
                                                                                                                                                                                                                                                                                                                                                  EILAPPNGSVPGDRITFDAF-PGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    452 EPLDPPAGSAPGERVFVKGYEKGQPDEELKPKKKVFEKLQADFKISDEYIAQWKQTNFMT 511
                                --KEKIEKKG 131
                                                                                             EFVILRDEKWGGNKTYTAYLDLEKDFADEVV-HPGDLKNSVEVALNKLLDPIREKFNTPA 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96133898; PubMed=8552597; DOI=10.1073/pnas.93.1.166; Ribas de Pouplana L., Frugier M., Quinn C.L., Schimmel P.; "Evidence that two present-day components needed for the genetic code appeared after nucleated cells separated from eubacteria."; Proc. Natl. Acad. Sci. U.S.A. 93:166-170(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYYC_HUMAN STANDARD; PRT; 527 AA.
P854577, 043276, 043276,
01-0CT-1996 (Rel. 34, Created)
25-0CT-2004 (Rel. 45, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Tyrosyl-tRNA synthetase, cytoplasmic (RC 6.1.1.1) (Tyrosyl--tRNA ligase) (TyrRS).
                                ENVI------QSTAVTTVSSGTKEQIKGGTGDEKKA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 K-GKGVCRA 303
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=12477973; DOI=10.1073/pnas.242611799;
Yang X.L., Skene R.J., McRee D.B., Schimmel P.;
"Crystal structure of a human aminoacyl-tRNA synthetase cytokine.";
Proc. Natl. Acad. Sci. US.A. 99:15369-15374 (2002).
-! - CATALYTIC ACTIVITY: ATP + L-tyrosine + tRNA(Tyr) = AMP +
diphosphate + L-tyrosyl-tRNA(Tyr).
-! - SUBCELDULAR LOCATION: Cytoplasmic.
-! - SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
                                                                                                                                                                                                  MEDLINE-222608298, PubMed=12665801; DOI=10.1038/nbt810; Gevaert K., Goethals M., Martens L., Van Damme J., Staes A., Thomas G.R., Vandekerckhove J.; "Exploring proteomes and analyzing protein processing by mass spectrometric identification of sorted N-terminal peptides."; Nat. Biotechnol. 21:566-569(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: Contains 1 tRNA-binding domain.
-1- CAUTION: Ref.1 sequence differs from that shown due to frameshift in position 353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GG: GO: GOOS STATE C: CYTOPLASH, TAS.

GG: GO: GO: GOOS STATE C: CYTTACELLULAT Space; TAS.

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GG: GO: GO: GO: STATE C: CONTROLL SPACE; TAS.

INTERPRO: IPRO02994; Nucleic_acid_OB.

INTERPRO: IPRO02905; TANA-SYNT_I.

INTERPRO: IPRO02507; TAY ERNA-SYNT_I.

INTERPRO: IPRO02507; TAY ERNA-SYNT_I.

REAL PRO1589; TRNA-SYNT_I.

Sci. U.S.A. 99:16899-16903(2002)
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PROSITE; PS00178; AA TRNA_LIGASE_I; FALSE_NEG.
PROSITE; PS50886; TRBD; 1.
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"HIGH" region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-15, AND ACETYLATION SITE GLY-1.
TISSUE=B-cell lymphoma;
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Unpublished observations (OCT-2004).
[6]
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PDB; INTG; X.ray; A=1-371.
PDB; IQ11; X.ray; A=1-371.
Genew; HGNC:12840; YARS.
H-InvDB; HIX0000381; -.
MIM; 603623; -.
GO; GO:0005737; C:cytoplasm; TAS.
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tRNA-binding.
INIT MET 0 0 0
MOD RES 1 1
Proc. Natl. Acad.
                                                                                                                                                                     rissum=Platelet;
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 230 ASSP---EKIEILAPPNGSVPGDRITFDAF-PGEPDKELNPKKIMEQIQPDLHTNDECV 285

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Search completed: August 3, 2005, 21:57:20 Job time: 177 secs

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GenCore version 5.1.6
(c) 1993 -- 2005 Compugen Ltd.
                  Copyright
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- protein search, using sw model OM protein

Run on:

August 3, 2005, 21:46:39 ; Search time 41 Seconds (without alignments) 732.186 Million cell updates/sec

US-10-623-567A-1 1573 1 MANNDAVLKRLEQKGAEADQ......FEVKGKGVCRAQTMSNSGIK Perfect score: ritle:

Sequence:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

fotal number of hits satisfying chosen parameters: Searched:

Minimum

seq length: 0 seq length: 2000000000 88 Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl: * 2: pirl: * 3: pirl: * 4: pir4: * PIR 79:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

probable tRNA synt probable tRNA synt hypothetical 12.3 methionine-tRNA 11 methionine-tRNA 11 methionine-tRNA 11 methionine-tRNA 11 methionine-tRNA 11 methionyl-tRNA syn methionyl-tRNA li methionyl-tRNA syn methionyl-tRNA syn methionyl-tRNA syn methionyl-tRNA syn methionine-tRNA li ARC1 protein - yea probable methionyl hypothetical prote methionyl-tRNA syn methionine-tRNA li endothelial monocy endothelial monocy hypothetical prote SUMMARIES A55053 A55083 A55083 T05247 T05247 T47822 T47822 T47822 T47822 B75074 B75074 B75074 B75074 B75074 B75075 B7128 F64457 F64457 F64457 F75395 F75 8 Length 110 658 629 650 651 811 660 656 Query Match 31.7 227.3 227.3 21.8 21.8 113.0 113.0 112.6 112.6 Result Š.

methionine-tRNA li	CsaA protein PA322	methionine-tRNA li	methionine-tRNA li	protein secretion	methionine-tRNA li	methionine-tRNA li	methionine-tRNA li	methionine-tRNA li	methionyl-tRNA syn		methionine tRNA sy	methionyl-tRNA syn	methionine-tRNA li	hypothetical prote	methionine-tRNA sy
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ALIGNMENTS

activa

thelial-monocyte

cursor (pro-EMAP II)

, M.L.; Grikscheit, T.;

9-Dec-2002

RES BS5	RESULT 1 BS5053 endothelial mo	
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. n	Biol. Chem. 26	25106-25119, 1994
A,A	A; Title: Characteriza A; Reference number:	Characterization of a novel tumor-derived cycokine. Endovice number: A55053; MUID:95014290; PMID:7929199
A;A	Accession: I Status: prel	155053 .iminary
A A	A; Molecule type: mRNA A: Residues: 1-310 < KAO>	
	Tross-refere	A; Cross-references: GB:U10117 C; Superfamily: endothelial monocyte-activating polypeptide II prec
Omz	Query Match Best Local Sin Matches 309;	Similarity 99.0%; Score 1546; DB 2; Length 310; Similarity 99.0%; Pred. No. 1.9e-87; Conservative 0; Mismatches 1; Indels ;
ò	1	MANNDA VLKRLEQKGAEADQI I EYLKQQVSLLKEKA I LQATLREBKKLRVE
ф	1	MANNDAVLKRIEQKGAEADQIIEYLKQQVSLLKEKAILQATLREEKKLRVEI
ò	61	ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEK
q	61	ELKQELIQAEIQNGVKQIRFPSGTPLHANSMVSENVIQSTAVTTVSSGTKE
È	121	KKAKEKI EKKGEKKEKKQOS I AGSADSKPIDVSRLDLRI GCI I TARKHPDA
đ	119	KKAKEKIEKKGEKKEKKQOSIAGSADSKPIDVSRLDLRIGGIITARKHPDA
8	181	VGEIAPRTVVSGLVMHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCAS:
q	179	VGETAPRITVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCAS
ò	241	PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGV
đ	239	PPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGV
ò	301	CRACTMSNIK 312
Д	299	CRAQTMSNSGIK 310

DSLYVEEVD 178

240

SPEKIEILA

SPEKIEILA 238

300 298

PFEVKGKGV |||||||||||

120

9 9

NAKLKKEIE QIKCCTCDE

NAKLKKEIE 2; Gaps

QIKG--CDE 118 DSLYVEEVD 180

RESULT

A55053
endochblial monocyte-activating protein II precursor - mouse
endochblial monocyte-activating protein II precursor - mouse
(2,Species: Mus musculus (house mouse)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004

N

8

Gaps

32;

Indels

677 117 173

-----TPTSTPASGIITE-----

233

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CjAccession: T05247
R;Bevan, M.; Weber, N.; Grueninger, D.; Schmidheini, T.; Bancroft, I.; Mewes, H.W.; Mayen Bubmitted to the Protein Sequence Database, February 1999
A;Reference number: 215405
A;Accession: T05247
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-797 cBEv>
A;Experimental source: cultivar Columbia; BAC clone F18A5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 4
A;Introns: 40/1; 88/2; 139/3; 191/3; 268/3; 316/3; 347/1; 382/3; 423/1; 460/3; 482/3; 52
A;Note: F18A5.170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                124 KEKIEKKGEKKEKKÇQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEVDVGE 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 EKIEILAPPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPF 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        methionine-tRNA ligase homolog F18A5.170 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999_#text_change 09-Jul-2004
                                                                                                                                                   779 LYVEQIDVGESAPRTVVSGLVRHVPLDQMQNRLVVVLCNLKPAKMRGVESRAMYMCASSP
                                                                                                                                                                                                                                            EELKQELIQAEIQNGVKQIAFP--SGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGT
                                                                                                                                                                                                                                                                                                                                                                                           118 GDEKKAKEKIEKKGEKKEKKQQSIAGSADSKP----IDVSRLDLRIGCIITARKHPDADS
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                                                                                                   1 MANNDAVLKRLEQKGAEADQII-EYLKQQVSLLKEKAILQATLREEKKLRVENAKLKKEI
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N;Alternate names: G4P1 protein; protein G3085; protein YGL105w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Superfamily: methionyl-tRNA synthetase, dimer-forming
Best Local Similarity 42.3%; Pred. No. 6e-27; Matches 135; Conservative 52; Mismatches 100;
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678 KTLQHQLIBLETAAGIKQVPKPVVSCTP-
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KVSSISNGTIR 797
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C;Species: Caenorhabditis elegans
C;Species: DS-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22898
R;Harris, B.
submitted to the EMBL Data Library, May 1996
A;Reference number: 219633
A;Accession: T22898
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DAA
A;Residues: 1-917 <WILL>
A;Cross-references: UNIPROT:Q20970; EMBL:Z73427; PIDN:CAA97803.1; GSPDB:GN00022; CESP:F5
A;Experimental source: clone FSBB3
C;Genetics:
A;Gene: CESP:F5BB3.5
A;Map position: 4352, 620/1; 655/1; 874/3
A;Introns: 27/2; 135/2; 620/1; 655/1; 874/3
C;Superfamily: methionyl-tRNA synthetase, dimer-forming
                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-310 < KAO.
A; Residues: 1-310 < KAO.
A; Residues: 1-310 < KAO.
A; Cross-references: UNIPROT: P31230; GB:U10118; NID:g498911; PIDN:AAA62203.1; PID:g498912
R; KAO., J: Brett, G: Chen, J:; Shen, H:; Fan, Y:G.; Godman, G.; Familletti, F
J. Biol. Chem. 267, 20239-20247, 1992.
A; Title: Endothelial monocyte-activating polypeptide II. A novel tumor-derived polypepti
A; Reference number: A44032; MUID:93015897; PMID:1400342
A; Residues: 145-158, X., 160-164 < KA2.>
A; Residues: 145-158, X., 160-164 < KA2.>
A; Residues: 145-158, X. Inc. 160-164 < KA2.
A; Residues: 145-164 < KA2
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C;Accession: A55053; A44032
R;Kao, J.; Houck, K.; Fan, Y.; Haehnel, I.; Libutti, S.K.; Kayton, M.L.; Grikscheit,
J.; Stern, D.M.
J. Biol. Chem. 269, 25106-25119, 1994
A;Title: Characterization of a novel tumor-derived cytokine. Endothelial-monocyte aci
A;Afele: cnamer: A55053; MUID:95014290; PMID:7929199
A;Accession: A55053
A;Stetus: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELKQELIQAEIQNGVKQIAFPSGTPLHANSMVSENVIQSTAV-TTVSSGTKEQIKGGTGD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 EKKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVEEV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVGEIAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEIL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 APPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELKOELILAEIHNGVEOVRVRLSTPLOTNCTASESVVOSPSVATTASPATKEOIK--AGE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MANNDAVLKRIEOKGAEADQIIEYLKOOVSLLKEKAILQATLREEKKLRVENAKLKKEIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85.4%; Score 1343; DB 2; Length 3
85.9%; Pred. No. 4.7e-75;
ive 13; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.9%
Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 VCRAQTMSNSGIK 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VCRAQTMANSGIK 310
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Length 797;

241

DB 2; Length 917;

35.9%; Score 564;

Query Match

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226

261

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A;Residues: 1-440 <STO>
A;Cross-references: UNIPROT:Q?XJM9; GB:AE002093; NID:g4895232; PIDN:AAD32818.1; GSPDB:GN
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F24G16.250 - Arabidopsis thaliana ($\text{Species}$: Arabidopsis thaliana (mouse-ear cress)$
C;Species: Arabidopsis thaliana (mouse-ear cress)$
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 17-Feb-2003
C;Accession: T47822
R;D'Angelo, M:; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.; submitted the Protein Sequence Database, February 2000
A;Reference number: 224477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 3
A;Introns: 157/2; 226/3
A;Note: F24G16.250
C;Superfamily: endothelial monocyte-activating polypeptide II precursor (pro-EMAP II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 EKKQQSIAGSADSKP-----IDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 EKKK----PAEPEPAKKEAELSVSLLNIQVGLIRKAWKHPSADSLLVEBIDVGEDKVRQ 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEK--IEILAPPNGSV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDEKKAKEKIEKKGEKK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                        101 AVTTVSSGTKEQIKGGTGDEKKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIG
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                                                                                                                                                                                                                                                                                                                                                                                                         22 IEYLKQQVSLLKEKAILQATLRE-----EKKLRVE-NAKLKKEIEELKQELIQAEIQNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 PGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVC 301
                                                                                                                                                                                         A;Gene: At2g40660
A;Map position: 2
C;Superfamily: endothelial monocyte-activating polypeptide II precursor
                                                                                                                                                                                                                                                                                                    Length 440;
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                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AL138647
A;Experimental source: cultivar Columbia; BAC clone F24G16
A; Reference number: A84420; MUID: 20083487; PMID: 10617197
                                                                                                                                                                                                                                                                                              Query Match 25.5%; Score 400.5; DB 2; Best Local Similarity 35.6%; Pred. No. 2.5e-17; Matches 105; Conservative 45; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.8%; Score 343; DB 2;
37.8%; Pred. No. 4.6e-14;
tive 40; Mismatches 58;
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Matches 84; Conservative
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                              A;Accession: C84832
A;Status: preliminary
A;Molecule type: DNA
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C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence revision 17-May-1996 #text_change 09-Jul-2004
C;Date: 17-May-1996 #sequence revision 17-May-1996 #text_change 09-Jul-2004
C;Accession: S64113; 869425; 522744
R;Castegnoll, L.; Paoluzi, S.; Minenkova, O.
Submitted to the Protein Sequence Database, May 1996
A;Reference number: S64112
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residuae: 1-376 cCAS>
A;Everences: UNIPROT: P46672; EMBL: Z72627; NID: 91322647; PIDN: CAA96812.1; PID: 9132
A;Experimental source: strain S288C
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Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Os-reb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
Cispaces on: C84832
Ribin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; W.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. Nature 402, Nfi-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-376 <CAMS.
A;Cross-references: EMBL:X97644; NID:g1310710; PIDN:CAA66247.1; PID:g1310719
R;Simos, G:, Segref, A:; Fasiolo, F:; Hellmuth, K.; Shevchenko, A:; Mann, M.; Hurt, E.C.
EMBO J. 15, 5437-5448, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Title: The yeast protein Arcip binds to tRNA and functions as a cofactor for the methi
A,Reference number: S72274; MUID:97050848; PMID:8895587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Description: functions as a cofactor for methionyl- and glutamyl-tRNA synthetases C; Superfamily: endothelial monocyte-activating polypeptide II precursor (pro-EMAP II) C; Keywords: cytosol; homodimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ģ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 KKEIE---ELKQELIQABIQNGVKQIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQ 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 IKGGTGDE---KKAKEKIE-KKGEKK---EKKQQSIAGSADSKPIDVSRLDLRIGCIITA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 RKHPDADSLYVEEVDVG-EIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 AMVMCASSPEKIEILAPPNGSVPGDRITFDAFPGE-PDKELNPKKKIWEQIQPDLHTNDE 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 AMVLCGSNDDKVEFVEPPKDSKAGDKVFFEGFGDEAPMKQLNPKKKIWEHLQPHFTTNDG 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: EMBL:X95481; NID:g1620459; PIDN:CAA64750.1; PID:g1620460
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.3%; Score 429; DB 2; ilarity 42.7%; Pred. No. 3.7e-19; Conservative 32; Mismatches 81;
                                                                                                                                                                                                                                                                                                 R;Castagnoli, L.; Paoluzi, S.; Minenkova, O. submitted to the EMBL Data Library, April 1996 A;Reference number: $69417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Gene: SGD:ARC1; G4Pl
A,Cross-references: MIPS:YGL105w; SGD:S0003073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-376 <SIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 7L
C;Complex: homodimer
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: S72274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105;
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C;Species: Thermus aquaticus
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Dec-2002
C;Datession: A39517
C;Accession: A39517
R;Nureki, O.; Muramatsu, T.; Suzuki, K.; Kohda, D.; Matsuzawa, H.; Ohta, T.; Miyazawa, T
J. Biol. Chem. 266, 3268-3277, 1991
A;Title: Methionyl-tRNA synthetase gene from an extreme thermophile, Thermus thermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:M64273; GB:J05744; NID:g155135; PIDN:AAA27510.1; PID:g155136 A;Experimental source: strain HB8, ArCC 27634 A;Note: the authors translated the codon TAC for residue 323 as Thr C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Superfamily: methionyl-tRNA synthetase, dimer-forming
C;Keywords: aminoacyl-tRNA synthetase; ATP; homodimer; ligase; protein biosynthesis
F;13,19,50,300/Active site: Tyr, His, Asp, Lys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 IAPRIVVSGLVNHVPLEQMQNRMVILLCNLKPAKNRGVLSQAMVMCASSPEKIEILAPPN 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - BERTVVSGIAKWYRPEELVGKKVVLVANLKPAKLRGIESQGMILAAQEGEAL-ALVTVE 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                       550 D--EQIIYFILNYMGRNNPEGA-----KMLLEKYYKREDVIKVA----KEKF----GEESK 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IAPPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQI-----KGGTGDEKKAKEKIEKKG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        447 İASILLİPAMPDIM------AELRRALGLKEEVRLEEAERWGLAEPRPIPEEAPVLF 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKKEKKQQSIAGSADSKP-----IDVSRLDLRIGCIITARKHPDADSLYVEEVDVGE 183
                                                                                                                                                                                                                                                                                                                                                                   73 NGVKQIAF-----PSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE-- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---KKAKEKIEKKGEKKEKKQQSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 EVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKNRGVLSQAMVMCASSPEKIE 237
                                                                                                                                                                                                                                           20 QIIEYLKQOVSLLKEKAILQATLREEKKLRVENAKLKKEIEEL-----KQELIQAEIQ
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                                                                                                 48;
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    Length 723,
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                                                                                            Indels
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A;Accession: A39517
                                                                                            72:
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; Score 216; DB 2;
; Pred. No. 8.1e-06;
53; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N,Alternate names: methionyl-tRNA synthetase C,Species: Thermus aquaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          methionine-tRNA ligase (EC 6.1.1.10)
         13.7%;
29.1%;
Query Match
Best Local Similarity 29.1<sup>†</sup>
Matches 71; Conservative
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709 LLMP 712
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D71091
methionine-tRNA ligase (EC 6.1.1.10) - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 16-Aug-2004
C;Accession: D71091
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekir
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA, Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: D71091
A;Sterus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-723 <KAW>
A;Residues: 1-723 <KAW>
A;Residues: 1-723 <KAW>
A;Residues: 1-723 <KAW>
A;Residues: 1-723 <KAW>
A;Residues: 1-723 <KAW>
A;Residues: 1-723 <KAW>
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Nolecule type: DNA
A;Residues: 1-723 <KAW>
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A;Residues: 1-723 <
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: BSD074
A;Description: Pyrococcus abyesi genome sequence: insights into archaeal chromosome stru
A;Accession: B75074
A;Status: preliminary
A;Accession: B75074
A;Status: DNA
A;Residues: 1-722 <KAW>
A;Coss-references: UNIPROT: Q9V011; GB:AJ248286; GB:AL096836; NID:g5458366; PIDN: CAB4989
C;Genetics: atrain Orsay
C;Genetics: A;Gene: metS; PAB2364
C;Superfamily: methionyl-tRNA synthetase, dimer-forming
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methionyl-tRNA synthetase (mets) PAB2364 - Pyrococcus abyssi (strain Orsay)
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C;Superfamily: methionyl-tRNA synthetase, dimer-forming
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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larity 29.7%; Pred. No. 2.8e-06;
Conservative 52; Mismatches 75; Indels
                                                                :|| :|| |: |: |: |
MWELVQPLLKTDASGVSMLKEHLMRT-SSGLVTSKSLRNANI 272
                  IWEQIOPDIHINDECVATYKGVPFEVKGKGVCRAQTMSNSGI 311
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SQGMLLAADDGERVALLMP 711
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Matches 77
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C; Accession: G65095

R; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co. R; Rose, D.G.; Mau, B.; Shao, Y.
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A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
A; Accession: G65095
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C; Species: Archaeoglobus fulgidus
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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C; Carcham, R.D.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
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A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
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A; Reference number: A69250; MUID:98049343; PMID:9389475
A; Reference number: A69250; MUID:98049343; PMID:9389475
A; Returus: preliminary; nucleic acid sequence not shown; translation not shown
A; Residues: 1-658 «KME>
A; Residues: 1-658 «KME>
A; Residues: 1-658 «KME>
A; Cross-references: UNIPROT:028819; GB:AE001003; GB:AE000782; NID:g2689326; PIDN:AAB8979
C; Superfamily: methionyl-tRNA synthetase, dimer-forming
C; Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P42589; GB:AE000389; GB:U00096; NID:g1789451; PIDN:AAC76109.
A;Experimental source: strain K-12, substrain MG1655
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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 194.5; DB 2;
; Pred. No. 1.9e-05;
27; Mismatches 32;
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27.5%; Pred, No. 0.00024;
tive 49; Mismatches 94;
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A,Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                 D.J.; Mayhew
                                                                                                                                                                                                                                                                                                                                                                                                                     K.; Apodaca
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hypothetical 12.3 kD protein in ileX-ebgR intergenic region - Escherichia coli (strain
C;Species: Escherichia coli
                                                                                                                                                                    (strain 0157:H7, substrain
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                                                                                                 probable tRNA synthetase ygjH [imported] - Escherichia coli (strain O157:H7, C;Species: Bscherichia coli (5 Date: 16 Feb-2001 #sequence_revision 16 Feb-2001 #text_change 09-Jul-2004 C;Accession: C55968 R;Perna, N.T.; Plunkett III G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grocheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001 A;Hitle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Accession: C55968
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A,Gene: ygjH
C,Superfamily: secretion chaperone CsaA
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C,Superfamily: secretion chaperone CsaA
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Best Local Similarity
Matches 43; Conserva
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A;Molecule type: DNA
A;Residues: 1-110 <STO>
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Gaps

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RESULT 15
E72297
methionine-tRNA ligase (EC 6.1.1.10) - Thermotoga maritima (strain MSB8)
C; Species: Thermotoga maritima
C; Decies: Thermotoga maritima
C; Decies: Thermotoga maritima
C; Decies: Thermotoga maritima
C; Decies: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C; Accession: E72297
R; Melson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C, M.
Nature 399, 323-329, 1999
A; Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A; Reference number: A72200; MUID:99287316; PMID:10360571
A; Residues: 1-629 <ARNA
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11.8%; Score 185.5; DB 2; Length 629;
Best Local Similarity 26.2%; Pred. No. 0.0005;
Matches 50; Conservative 46; Mismatches 72; Indels 23.
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Search completed: August 3, 2005, 21:58:05 Job time: 42 secs
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                                                                                                                                                                                                                             The invention provides an anti-tumour and anti-angiogenic agent of p43 consisting of two domains, the N-terminal domain (146 amino acids) and creminal domain (166 amino acids) containing 11 beta-strands forming a structural core and 3 flanking alpha-helices. p43 is useful as an anti-tumour and anti-angiogenic agent. p43 and its C-terminal cytokine domain (EMAP II) induce regression of fibrosarcoma in immunocompromised mouse while its N-terminal domain does not. p43 is a potent cytokine as determined by the induction of tumour necrosis factor-alpha (TNF-alpha), interleukin-6 (IL-6), IL-8 and matrix metalloprotease-9 or by its activity of chemotaxis. The present sequence represents the human p43, polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELKOELIQAEIQNGVKQIAPPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE 120
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                                                                                                                                                                    anti-tumor and anti-angiogenic agent of p43 comprises N-terminal
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                                                                                                                                                                              domain and C-terminal domain containing eleven beta-strands forming a structural core and three flanking alpha-helices.
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                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                             Claim 1; Fig 1; 35pp; English.
                                                    14-JUN-2000; 2000WO-KR000630
                                                                        14-JUN-2000; 2000WO-KR000630
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Matches 312; Conservative
                                                                                            (IMAG-) IMAGENE CO LTD
                                                                                                                 Ko Y, Kim YS,
                                                                                                                                    WPI; 2002-098017/13.
N-PSDB; ABA94640.
                                                                                                                                                                                                                                                                                                                                                             Sequence 312 AA;
           WO200195927-A1
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                                                                                                                 Kim S,
                                                                                                                                                                    Novel
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diagnosing, staging, monitoring, prognosticating, preventing, treating or determining the predisposition to diseases or conditions such as prostate cancer. They may be used as molecular markers, drug targets, vaccines, in gene therapy, research, clinical medicine or forensic science. The present sequence is a differentially regulated prostate protein (endothelial monocyte activating polypeptide II), Pc240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide for diagnosing, staging, monitoring, prognosticating, preventing or treating, or determining the predisposition to, diseases or conditions such as prostate cancer, and for research or forensic science.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel differentially regulated genes and polypeptides encoded by them. Sequences of the invention are useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELKOELIQAEIONGVKOIAPPSGTPLHANSMVSENVIOSTAVTTVSSGTKEQIKGGTGDE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKAKEKIEKKGEKKEKKQOSIAGSADSKPIDVSRLDLRIGCIITARKHPDADSLYVBEVD 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MANNDAVLKRLEQKGAEADQIIEYLKQQVSLLKEKAILQATLRESKKLRVENAKLKKEIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELKOELIQAEIONGVKOIAFPSGTPLHANSMVSENVIQSTAVTTVSSGTKEQIKGGTGDE
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Human, differentially regulated protein; prevention; therapy; va
prostate cancer; endothelial monocyte activating polypeptide II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1573; DB 6; 100.0%; Pred. No. 1.6e-135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kovace KF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ORIG-) ORIGENE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                              07-NOV-2001, 2001US-0331041P.
07-NOV-2001, 2001US-0331042P.
18-DEC-2001, 2001US-0340251P.
07-JAN-2002, 2002US-0344791P.
                                                                                                                                                                                                                                                                                                                                       07-NOV-2002; 2002WO-US035563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 312, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Li X, Jay G,
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                                                                     gene therapy; Pc240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAL60070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 312 AA;
                                                                                                                                                                                                      WO2003040331-A2
                                                                                                                                       Homo sapiens
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RESULT 3

AA029575 standard; protein; 312 AA

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